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OM nucleic - nucleic search, using sw model

Run on: September 1, 2004, 20:41:05 ; Search time 2748 Seconds
(without alignments)
9943.088 Million cell updates/sec

Title: US-10-030-390-2

Perfect score: 5497

Sequence: 1 gaattcgataagtcattt.....ctagtcgaagtgattaaata 5497

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3267054 seqs, 2485319735 residues

Total number of hits satisfying chosen parameters: 6534108

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

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- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	5010.8	91.2	5770	9	US-09-838-718A-7
2	5001.4	91.0	5906	9	US-09-838-718A-6
3	4999	90.9	5870	9	US-09-838-718A-8
4	4993.4	90.8	5230	9	US-09-838-718A-5
C 5	1434.8	20.1	3765	9	US-09-070-927A-287
C 6	1109.4	20.2	10929	15	US-10-032-393-7
C 7	876.6	15.9	9412	15	US-10-032-393-51
C 8	876.6	15.9	9412	15	US-10-032-393-52
C 9	876.6	15.9	9417	15	US-10-032-393-48
C 10	876.6	15.9	9425	15	US-10-032-393-46
C 11	876.6	15.9	9437	15	US-10-032-393-17
C 12	876.6	15.9	9484	15	US-10-032-393-49
C 13	876.6	15.9	9566	15	US-10-032-393-50
C 14	876.6	15.9	12733	15	US-10-032-393-47

C 15	876.6	15.9	12739	15	US-10-032-393-8
C 16	833.8	15.2	9749	9	US-09-070-927A-154
C 17	747	13.6	747	9	US-09-974-300-5684
C 18	731.6	13.3	738	10	US-09-989-643-114
C 19	381	6.9	381	9	US-09-974-300-1224
C 20	244.2	4.4	6405	10	US-09-869-855A-1
C 21	244.2	4.4	6837	10	US-09-928-847B-49
C 22	241	4.4	735	10	US-09-989-643-115
C 23	229.2	4.2	732	10	US-09-989-643-113
C 24	204	3.7	447	16	US-10-166-349-11
C 25	204	3.7	447	16	US-10-166-349-19
C 26	178.8	3.3	1650	16	US-10-338-221-2127
C 27	178.8	3.3	1716	16	US-10-338-221-6057
C 28	178.8	3.3	81905	16	US-10-338-221-2057
C 29	178.8	3.3	83689	16	US-10-338-221-11
C 30	174.6	3.2	6405	10	US-09-869-855A-1
C 31	174.6	3.2	6837	10	US-09-928-847B-49
C 32	143.2	2.6	5502	9	US-09-735-457-785
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C 34	143.2	2.6	5502	9	US-09-849-626-785
C 35	143.2	2.6	5502	10	US-09-476-300-785
C 36	143.2	2.6	5502	13	US-10-283-017-785
C 37	143.2	2.6	5502	15	US-10-017-754-785
C 38	143.2	2.6	5502	15	US-10-113-872-785
C 39	142.2	2.6	673	13	US-10-082-973-5
C 40	142.2	2.6	685	15	US-10-082-973-4
C 41	142.2	2.6	686	15	US-10-082-973-52
C 42	142	2.6	142	9	US-09-060-878-1
C 43	142	2.6	142	13	US-10-350-250-1
C 44	141.6	2.6	2290	10	US-09-935-280-16
C 45	140.8	2.6	4557	16	US-10-457-372-5

ALIGNMENTS

RESULT 1

US-09-838-718A-7
; Sequence 7, Application US/09838718A
; Patent No. US20020019043A1
; GENERAL INFORMATION:
; APPLICANT: Steidler, Lothar
; APPLICANT: Remaut, Erik R.
; APPLICANT: Fiers, Walter R.
; TITLE OF INVENTION: USE OF A CYTOKINE-PRODUCING LACTOCOCCUS STRAIN TO TREAT COLITIS
; FILE OF INVENTION: 2676-4779US
; CURRENT APPLICATION NUMBER: US/09/838,718A
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: PCT/EP99/07800
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: EP 98203529.7
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7
; LENGTH: 5770
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pT1MIL10
US-09-838-718A-7

Query Match 91.2%; Score 5010.8; DB 9; Length 5770;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5002; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	496	CTAACTAGTAGATCGGCTGCTAACAAAGCCGAAAGAGCTGAGTTGGCTGCTGCCAC	555
Db	769	CTAACTAGTAGATCGGCTGCTAACAAAGCCGAAAGAGCTGAGTTGGCTGCTGCCAC	828
Qy	556	CGCTGAGCAATACTAGCATAAACCCCTTGGGGCCCTCTAAACGGGTCTTGAGGGGTTTTTT	615
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Qy	616	GCTGAAAGGAGGAAC	TATATCCGGATGACCTGCAGGCAAGCTCTAGAAATCGATACGATTT	675
Db	889	GCTGAAAGGAGGAAC	TATATCCGGATGACCTGCAGGCAAGCTCTAGAAATCGATACGATTT	948
Qy	676	TGAAGTGGCAACAGAT	AAAAAAGCGATTTAAATTTGTCGTAACCTTTTAAAAAACAAGC	735
Db	949	TGAAGTGGCAACAGAT	AAAAAAGCGATTTAAATTTGTCGTAACCTTTTAAAAAACAAGC	1008
Qy	736	AAATACAATCATTTGT	CGCAACAGATACGACAGAGGCGAAAAACATTCCTCGTGGTCGAT	795
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Db	1069	CATTTCATAAAGCAAAA	TGCCCTTTTCTAAAGATATAAAACGTATAAAAGACTATGGATCAATAG	1128
Qy	856	TTTAGAAAAAGATGTGAT	CCGTAGCGGTTTCAAAATTTTCAACCCAGGGAATGAATTACTA	915
Db	1129	TTTAGAAAAAGATGTGAT	CCGTAGCGGTTTCAAAATTTTCAACCCAGGGAATGAATTACTA	1188
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Db	1189	TCCTCTTTTACAAGACG	GAAAGAAAAACGAAATGATACACCAATCAGTCGAAAAAAA	1248
Qy	976	GATATATGGAGATAAG	ACGGTTTCGTGTTTCGTGCTGACTTGCACCATATCATATAAAATC	1035
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Qy	1036	GAAACACGAAGAATG	CGGAAACGTHAAAGAGTTATGGAATATAGACTTAGAAGCAAA	1095
Db	1309	GAAACACGAAGAATG	CGGAAACGTHAAAGAGTTATGGAATATAGACTTAGAAGCAAA	1368
Qy	1096	CTTAAGAGTGTGTTGAT	GTAGTGCAGTATCTTTAAAAATTTGTATAATAGCAATTCGAAGTTAA	1155
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Qy	1336	GGCTAAAAATAGTAAA	ACAGGTAAACGCTTATTTGAATTAAGACAGTCACTATTTCAACTTTATC	1395
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2029	DB	GAAGCTATATACGTACTTTGTTTCAAAATGGGTCAAATCGAGAAATATCGTCAACTGTTTAC	2088
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2149	DB	TTATGACGAGTATGTCTATTTTTTAAATAGTTATCTATTATTTTAAACGGGAGGAAATAAAT	2208
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2209	DB	CTATGAGTCGCTTTTGTAAATTTGGAAGTTACACGTTACTTAAAGGGAATGTAGATAAAT	2268
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2329	DB	GGGGAAGCTCGGATCATATGCTAAAGACAAAATAAACTCGCAACGACACTTCGGAGAAATGGG	2388
2116	QY	ACGAATCGAGAAAACCCCTCTTTACGTGGATTACATATCTAATAAGACCGTAGGAGACG	2175
2389	DB	ACGAATCGAGAAAACCCCTCTTTACGTGGATTACATATCTAATAAGACCGTAGGAGACG	2448
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Db	2104	AAGTAAACAGTGTCTTAATAAATACTTACCGCCATACACAGATGTTCCAGATAAATAT	2163
Qy	1755	GGAAAGCTATATACGTACTTTGTTTCAAAATGGGTCAATCGAGAATATCGTCAACTGTTTA	1814
Db	2164	GGAAAGCTATATACGTACTTTGTTTCAAAATGGGTCAATCGAGAATATCGTCAACTGTTTA	2223
Qy	1815	CTAATAATCAGTTTCTCAAGCAATGAAACACGCCCAAGTAAACAATTTAAGTACCGTTTA	1874
Db	2224	CTAATAATCAGTTTCTCAAGCAATGAAACACGCCCAAGTAAACAATTTAAGTACCGTTTA	2283
Qy	1875	CTTATGAGCAAGTAATGCTTANTTTTAAATAGTTATCTATTTATTTAAACGGGAGAAATAAT	1934
Db	2284	CTTATGAGCAAGTAATGCTTANTTTTAAATAGTTATCTATTTATTTAAACGGGAGAAATAAT	2343
Qy	1935	TCATGAGTCCGTTTGTAAATTTGAAATTTGAAAGTTACAGTTTACTTAAAGGGAATGTAGTAA	1994
Db	2344	TCATGAGTCCGTTTGTAAATTTGAAATTTGAAAGTTACAGTTTACTTAAAGGGAATGTAGTAA	2403
Qy	1995	TTATTAGGTATATCTACTGACAGCTTCCAAGGAGCTAAAGAGTCCCTAGCGTCTTTATCA	2054
Db	2404	TTATTAGGTATATCTACTGACAGCTTCCAAGGAGCTAAAGAGTCCCTAGCGTCTTTATCA	2463
Qy	2055	TGGGGAAGCTCGGATCATATGCAAGACAAATAAATCTCGCAACAGCACATTGAGAAATGG	2114
Db	2464	TGGGGAAGCTCGGATCATATGCAAGACAAATAAATCTCGCAACAGCACATTGAGAAATGG	2523
Qy	2115	GACGAATCGAGAAACCCCTTTACGCTGGATTACATATCTAATAAGCCGTAAAGGAGAC	2174
Db	2524	GACGAATCGAGAAACCCCTTTACGCTGGATTACATATCTAATAAGCCGTAAAGGAGAC	2583
Qy	2175	GGGTTCAAAAAGTTTAAATFAAAGGAGAGCAATCAATGCAATPAGTAGAATATATTTT	2234
Db	2584	GGGTTCAAAAAGTTTAAATFAAAGGAGAGCAATCAATGCAATPAGTAGAATATATTTT	2643
Qy	2235	TTGGACACGCTGGAGAAATTTAGAGACGCTCTCCAAAGACAGTTTACAAAGAGCTAGTG	2294
Db	2644	TTGGACACGCTGGAGAAATTTAGAGACGCTCTCCAAAGACAGTTTACAAAGAGCTAGTG	2703
Qy	2295	CACATAACATAATTTAATGCTATTAAGTGTGTGGAACTATATATATGGAATAAGCCG	2354
Db	2704	CACATAACATAATTTAATGCTATTAAGTGTGTGGAACTATATATATGGAATAAGCCG	2763
Qy	2355	TAGAAGATTAAGCAAGAGGAGAAATTTAGAGAGAAATTTAATGCAATATGCGTGGCCGT	2414
Db	2764	TAGAAGATTAAGCAAGAGGAGAAATTTAGAGAGAAATTTAATGCAATATGCGTGGCCGT	2823
Qy	2415	TAGATGGGAACATATCAATTTTCTGGAGAAATGAAATTTGAAGATTTACATGACACTG	2474
Db	2824	TAGATGGGAACATATCAATTTTCTGGAGAAATGAAATTTGAAGATTTACATGACACTG	2883
Qy	2475	GGCAATGAAATTTACGCTCTTTACGTAATAAGAGCGGTTTTATCTTAATATAACGGCT	2534
Db	2884	GGCAATGAAATTTACGCTCTTTACGTAATAAGAGCGGTTTTATCTTAATATAACGGCT	2943
Qy	2535	CTTTTATAGAAAATTCCTTAGCGTGTGTTTTTTCGAAATGCTGGCGTACCCCAAG	2594
Db	2944	CTTTTATAGAAAATTCCTTAGCGTGTGTTTTTTCGAAATGCTGGCGTACCCCAAG	3003
Qy	2595	ATTAGAAATGAGTAGATCAAAATTTTACCAATAGAAATCAGGAAATTCAGATCCAAACCAT	2654
Db	3004	ATTAGAAATGAGTAGATCAAAATTTTACCAATAGAAATCAGGAAATTCAGATCCAAACCAT	3063
Qy	2655	AAAAACTAGAACAAATTCGAAAGTTAATCACTCAAGCTAGTAGTGATTTATCCC	2714
Db	3064	AAAAACTAGAACAAATTCGAAAGTTAATCACTCAAGCTAGTAGTGATTTATCCC	3123
Qy	2715	AAATGAGCCACAGAACCCAGAGCCAGAAACAGAAATCAGAACTAAGTAACTTGGATTAGA	2774
Db	3124	AAATGAGCCACAGAACCCAGAGCCAGAAACAGAAATCAGAACTAAGTAACTTGGATTAGA	3183
Qy	2775	AATGGAAGAGAAAAAGCAATGACTTCTGTTGAATTAATGACGAAATCGTTGCTTATTT	2834
Db	3184	AATGGAAGAGAAAAAGCAATGACTTCTGTTGAATTAATGACGAAATCGTTGCTTATTT	3243
Qy	2835	TTTTTTAAAGCGGTATACATAGATATAACGAAACCAACGAACTGAATAGAAACGAAAAAG	2894
Db	3244	TTTTTTAAAGCGGTATACATAGATATAACGAAACCAACGAACTGAATAGAAACGAAAAAG	3303
Qy	2895	AGCCATGACACATTTATAAAATGTTTGACGACATTTTATAAATGCATAGCCCGATAAGAT	2954
Db	3304	AGCCATGACACATTTATAAAATGTTTGACGACATTTTATAAATGCATAGCCCGATAAGAT	3363
Qy	2955	TGCCAAACCAACGCTTATACATAGTCAGATGAATCTCTTCCCTCGTAAGAAATTTATTAA	3014
Db	3364	TGCCAAACCAACGCTTATACATAGTCAGATGAATCTCTTCCCTCGTAAGAAATTTATTAA	3423
Qy	3015	TTAACTTTGTTTGAAGCGGTATATAACCGTACTATCATTTATATAGGGAATCAGAGAGT	3074
Db	3424	TTAACTTTGTTTGAAGCGGTATATAACCGTACTATCATTTATATAGGGAATCAGAGAGT	3483
Qy	3075	TTTCAAGTATCTAAGCTACTCAATTTTAAGAAATGTTTAAGCAATCAATCGGAAATCGTTTG	3134
Db	3484	TTTCAAGTATCTAAGCTACTCAATTTTAAGAAATGTTTAAGCAATCAATCGGAAATCGTTTG	3543
Qy	3135	ATTGCTTTTTTTGTTATTTTATTTATAGAGGTGGAGTTTGTATGATCATGATGAATGTAA	3194
Db	3544	ATTGCTTTTTTTGTTATTTTATTTATAGAGGTGGAGTTTGTATGATCATGATGAATGTAA	3603
Qy	3195	AACTTATATAAAAAATAGTTTATTTGGAGATAAGAAAAATTAGCAAAATCTATACACTAGA	3254
Db	3604	AACTTATATAAAAAATAGTTTATTTGGAGATAAGAAAAATTAGCAAAATCTATACACTAGA	3663
Qy	3255	AACGTTTAAAGAAAGAGTTAGAAAAAGAGAAATATCTACTTAGAAAAAATAATCAGATAAGTA	3314
Db	3664	AACGTTTAAAGAAAGAGTTAGAAAAAGAGAAATATCTACTTAGAAAAAATAATCAGATAAGTA	3723
Qy	3315	TTTTTTCTCGAGGGGAGGATTTATATATAAGTTTAAATGAAAAATAACAAAAATAATTA	3374
Db	3724	TTTTTTCTCGAGGGGAGGATTTATATATAAGTTTAAATGAAAAATAACAAAAATAATTA	3783
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Db	3784	TTGATTTAGTGGAAAAAATTTGACTTATAAGGAAAAAATCTTTTTCAAAAACATGCAAT	3843
Qy	3435	ATTGGAACAGTTGATGAAAGGAAACCAAGTTTAAATTAACAACCTATTTTATAGGAT	3494
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Qy	3495	TATAGAAAGGAGAACAGCTGAATGAATATCCCTTTTGTGTAGAAAACTGTGCTTCATGA	3554
Db	3904	TATAGAAAGGAGAACAGCTGAATGAATATCCCTTTTGTGTAGAAAACTGTGCTTCATGA	3963
Qy	3555	CGGCTTGTAAAGTACAAATTTTAAATTAAGTAAATTCGCTCAATCACTACCAAGCCAGG	3614
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Qy	3735	ACCCAAAGCTTTTATGTTATGAAACGATGACAGAAAAACCGTTTATACACGAAAGGACA	3794
Db	4144	ACCCAAAGCTTTTATGTTATGAAACGATGACAGAAAAACCGTTTATACACGAAAGGACA	4203
Qy	3795	TTCTGAAAAACAAATTTAAGACAAATCAATACCTTTTATTTGATTTTGTATTTTACACGGC	3854
Db	4204	TTCTGAAAAACAAATTTAAGACAAATCAATACCTTTTATTTGATTTTGTATTTTACACGGC	4263

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RESULT 3
US-09-838-718A-8
; Sequence 8, Application US/09838718A
; Patent No. US20020019043A1
; GENERAL INFORMATION:
; APPLICANT: Steidler, Lothar
; APPLICANT: Remaut, Erik R.
; APPLICANT: Fiers, Walter R.
; TITLE OF INVENTION: USE OF A CYTOKINE-PRODUCING LACTOCOCCUS STRAIN TO TREAT COLITIS
; FILE REFERENCE: 2676-4779US
; CURRENT APPLICATION NUMBER: US/09/838,718A
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: PCT/EP99/07800
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: EP 98203529.7
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 5870
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pTIR5AH
US-09-838-718A-8

Query Match 90.9%; Score 4999; DB 9; Length 5870;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 4999; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2659 ACCTTAGAACAAATTTGAAAGTTAACTAACTCAACGCTAGTAGTGGATTTAATCCCAAT 2718
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Qy	4939	TTAAACAAGCTAGCAGAACCCCTTAAACCGGACACACAACTCGATTGTTTACGTATGAT	4998
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Qy	4999	ACAGGCTGAAAAATAAAACCCGCACTATGCCATTACATTTATCTATGATACGTTTGT	5058
Db	5372	ACAGGCTGAAAAATAAAACCCGCACTATGCCATTACATTTATCTATGATACGTTTGT	5431
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Db	5672	AGCATAATAGATTTATTGAATAGTCATTTAAAGTTGAGCATATTAGAGGAGGAAAAATCTTT	5731
Qy	5359	GGAGAAATATTTGAAGAACCGGATTACATGGATTGGATTAGTCTTCTGTGTACGCGGTT	5418
Db	5732	GGAGAAATATTTGAAGAACCGGATTACATGGATTGGATTAGTCTTCTGTGTACGCGGTT	5791
Qy	5419	TTTAACTTAAAGTAGTGAAATTTTGTGATTTTGGTGCTGTGTCTTGTGTTAGTATTTCG	5478
Db	5792	TTTAACTTAAAGTAGTGAAATTTTGTGATTTTGGTGCTGTGTCTTGTGTTAGTATTTCG	5851
Qy	5479	TAGTCAAAGTGATTTAAATA	5497
Db	5852	TAGTCAAAGTGATTTAAATA	5870

RESULT 4

```

US-09-838-718A-5
; Sequence 5, Application US/09838718A
; Patent No. US20020019043A1
; GENERAL INFORMATION:
; APPLICANT: Steidler, Lothar
; APPLICANT: Remaut, Erik R.
; APPLICANT: Fiers, Walter R.
; TITLE OF INVENTION: USE OF A CYTOKINE-PRODUCING LACTOCOCCUS STRAIN TO TREAT COLITIS
; FILE REFERENCE: 2676-4779US
; CURRENT APPLICATION NUMBER: US/09/838,718A
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: PCT/EP99/07800
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: EP 98203529.7
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5230
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pTREX1
US-09-838-718A-5

```

Query Match 90.8%; Score 4993.4; DB 9; Length 5230;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4997; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
495 TCTAACTAGTAGATCCGGCTGCTATCAAAAGCCGAAAGAGCTGAGTGTGCTCTGCCA 554

228 TCTCTAGAAATGGATCCGGCTGCTTAAACAAAGCCGAAAGAAAGCTGAGTTGGCTGCTGGCCA 287

555 CGCGTGAACAATAACTAGCATAAACCCCTTTGGGGCCCTCTAAACGGGTCTTTGAGGGGTTTTT 614

288 CGCGTGAACAATAACTAGCATAAACCCCTTTGGGGCCCTCTAAACGGGTCTTTGAGGGGTTTTT 347

615 TCGTCAAGAGGAGAACTATATCCGATGACCTGCGAGGCAAGCTCTAGAAATCGATACGATT 674

348 TCGTCAAGAGGAGAACTATATCCGATGACCTGCGAGGCAAGCTCTAGAAATCGATACGATT 407

675 TTGAAGTGGCAACAGATAAAAAAAGCAGTTTAAAAATTTGTTGCTGAACATTTTAAACCAAG 734

408 TTGAAGTGGCAACAGATAAAAAAAGCAGTTTAAAAATTTGTTGCTGAACATTTTAAACCAAG 467

735 CAAATACAAATCAATTTGTCGAAACAGATAGCGACAGAGAGGCGAAAAACATTTGCCTGTCGCA 794

468 CAAATACAAATCAATTTGTCGAAACAGATAGCGACAGAGAGGCGAAAAACATTTGCCTGTCGCA 527

795 TCATTCATAAAGCAAAATGCGCTTTTCTAAAGATAAAACCGTATAAAGAGACTATGGATCAATA 854

528 TCATTCATAAAGCAAAATGCGCTTTTCTAAGATAAAACCGTATAAAGAGACTATGGATCAATA 587

855 GTTTAGAAAAAGATGTGATCCGTAGCGGTTTCTAAAAATTTGCAACCGAGGAATGAATTACT 914

588 GTTTAGAAAAAGATGTGATCCGTAGCGGTTTCTAAAAATTTGCAACCGAGGAATGAATTACT 647

915 ATCCCTCTTTTCAAGAGCGCAAAAGAAAAACGAAATGATACACCAATCAGTGCAAAAA 974

648 ATCCCTCTTTTCAAGAGCGCAAAAGAAAAACGAAATGATACACCAATCAGTGCAAAAA 707

975 AGATATAATGGAGATAAGACGGTTCTGCTGTTCTGCTGCACTTGCAACCATATCATAAAAAT 1034

708 AGATATAATGGAGATAAGACGGTTCTGCTGTTCTGCTGCACTTGCAACCATATCATAAAAAT 767

1035 CGAAACACCAAGAAATCGCGGAAACCGTAAAGAGGTATGGAATTAAGACTTAGAGCAA 1094

768 CGAAACACCAAGAAATCGCGGAAACCGTAAAGAGGTATGGAATTAAGACTTAGAGCAA 827

1095 ACTTAAGAGTGTGTTGATAGTCAGATCTTAAAAATTTTGTAATAGGAATTTGAAGTTA 1154

828 ACTTAAGAGTGTGTTGATAGTCAGATCTTAAAAATTTTGTAATAGGAATTTGAAGTTA 887

1155 AATTAGATGCTAAAAAATTTGTAAATTAAGAGAGGTATTAATGAAACCAAAATATAAAAT 1214

888 AATTAGATGCTAAAAAATTTGTAAATTAAGAGAGGTATTAATGAAACCAAAATATAAAAT 947

1215 AATTCCTAAAAATTTTAAACAGGTGAAAAAGTACTCAACCAAAATATAAAACAAATTTGAAT 1274

948 AATTCCTAAAAATTTTAAACAGGTGAAAAAGTACTCAACCAAAATATAAAACAAATTTGAAT 1007

1275 TAAAGAAACCGCATACCGTTTACGAAATTTGAAACAGGTAAAGGGCATTTAACCGCAAAAC 1334

1008 TAAAGAAACCGCATACCGTTTACGAAATTTGAAACAGGTAAAGGGCATTTAACCGCAAAAC 1067

1335 TGGCTAAATTAAGTAACAGGTAAACGCTCTTAAATTTAGACAGTCACTCTATCAACTTTAT 1394

1068 TGGCTAAATTAAGTAACAGGTAAACGCTCTTAAATTTAGACAGTCACTCTATCAACTTTAT 1127

1395 CGTCAGAAAAATTTAAACTGAACTACTCGTGTCACTTTAAATTTCAACAGATATTTACAGT 1454

1128 CGTCAGAAAAATTTAAACTGAACTACTCGTGTCACTTTAAATTTCAACAGATATTTACAGT 1187

1455 TTCAATTCCTTAAACAAACAGAGGTATAAAATTTGTTGGGAGTATTCCTTACCAATTTAGCA 1514

1188 TTCAATTCCTTAAACAAACAGAGGTATAAAATTTGTTGGGAGTATTCCTTACCAATTTAGCA 1247

1515 CACAAATTTATTTAAAAAAGTGGTTTTTGAAGCCATCGCTCTGACATCTATCTGATTTG 1574

1248 CACAAATTTATTTAAAAAAGTGGTTTTTGAAGCCATCGCTCTGACATCTATCTGATTTG 1307

1575 AAGAAAGGAAATTTCAACAGGTACTCTCGATATTTCAACGAACTAGGGTTGCTCTTGACA 1634

1308	Db	AAGAAGGATTCTTCAAGACGGTACCTTTGGATATTCACCGAAACACTAGGGGTGCTCTTTGCACA	1367
1635	Qy	CTCAAGTCTCGATTTCAGCAATTTGCTTTAAGCTGCCAGCGGAATGCTTTTCATCCTTAAACCAA	1694
1368	Db	CTCAAGTCTCGATTTCAGCAATTTGCTTTAAGCTGCCAGCGGAATGCTTTTCATCCTTAAACCAA	1427
1695	Qy	AAGTAAACAGTGTCTTTAATAAACTTACCGCCCATACCAAGATGTTTCCAGATAAATATT	1754
1428	Db	AAGTAAACAGTGTCTTTAATAAACTTACCGCCCATACCAAGATGTTTCCAGATAAATATT	1487
1755	Qy	GGAAGCTATATACGTACTTTGTTTCAAAATGGGTCAATCGAGAATATCGTCAACTGTTTA	1814
1488	Db	GGAAGCTATATACGTACTTTGTTTCAAAATGGGTCAATCGAGAATATCGTCAACTGTTTA	1547
1815	Qy	CTAAAAATCAGTTTTCATCAAGCAATGAAACACGCCAAAGTAAACAAATTTAAGTACCGTTA	1874
1548	Db	CTAAAAATCAGTTTTCATCAAGCAATGAAACACGCCAAAGTAAACAAATTTAAGTACCGTTA	1607
1875	Qy	CTTATGAGCAAGTATTCGTATTTTAAATAGTTATCTATTATTAAACGGGAGGAATAAT	1934
1608	Db	CTTATGAGCAAGTATTCGTATTTTAAATAGTTATCTATTATTAAACGGGAGGAATAAT	1667
1935	Qy	TCTATGAGTCGCTTTTCTGTAATTTGAAAAGTTACACGTTACTAAAGGGAATGTAGATAAA	1994
1668	Db	TCTATGAGTCGCTTTTCTGTAATTTGAAAAGTTACACGTTACTAAAGGGAATGTAGATAAA	1727
1995	Qy	TTATTAGGTATACTACTGACAGCTTCCAGAGAGCTAAAGAGTCCCTAGCGCTCTTATCA	2054
1728	Db	TTATTAGGTATACTACTGACAGCTTCCAGAGAGCTAAAGAGTCCCTAGCGCTCTTATCA	1787
2055	Qy	TGGGAGAGCTCGGATCATATGCAAGACAAAATAAACTCCGCAACAGCACTTTGGAGAAATGG	2114
1788	Db	TGGGAGAGCTCGGATCATATGCAAGACAAAATAAACTCCGCAACAGCACTTTGGAGAAATGG	1847
2115	Qy	GAGCAATCGAGAAAAACCCCTCTTTACGCTGGATTACATATCTAATAAGCCGTTAAGGAGAC	2174
1848	Db	GAGCAATCGAGAAAAACCCCTCTTTACGCTGGATTACATATCTAATAAGCCGTTAAGGAGAC	1907
2175	Qy	GGGTTCAAAAAGGTTTAAATAAAGGAGAACCAATCAATGCATTAGCTAGAACTATATTTT	2234
1908	Db	GGGTTCAAAAAGGTTTAAATAAAGGAGAACCAATCAATGCATTAGCTAGAACTATATTTT	1967
2235	Qy	TTGGCAACCGTGAGAAATTTAGAGAACGTCCTCTCCAAGACCAAGTTTCAAAAGAGCTAGTG	2294
1968	Db	TTGGCAACCGTGAGAAATTTAGAGAACGTCCTCTCCAAGACCAAGTTTCAAAAGAGCTAGTG	2027
2295	Qy	CACATAACATAATTATTAAACGCTATAGTGTGGACACCTGTATATATCGGAAAAAGCCG	2354
2028	Db	CACATAACATAATTATTAAACGCTATAGTGTGGACACCTGTATATATCGGAAAAAGCCG	2087
2355	Qy	TAGAAGAAATTTAAAGCAAGAGGAGAAATTTAGAGAAGATTTTAAATGCCATATTCGCTGGCCGT	2414
2088	Db	TAGAAGAAATTTAAAGCAAGAGGAGAAATTTAGAGAAGATTTTAAATGCCATATTCGCTGGCCGT	2147
2415	Qy	TAGGATGGGAACATATCAATTTCTTGGAGAAATACAAATTTGAAGGATTCATCATGACACTG	2474
2148	Db	TAGGATGGGAACATATCAATTTCTTGGAGAAATACAAATTTGAAGGATTCATCATGACACTG	2207
2475	Qy	GGCAATGAAATTTACGTCCTTTACGTATAAAAGAGCGGTTTAAATCTTAAATAAAGCGCT	2534
2208	Db	GGCAATGAAATTTACGTCCTTTACGTATAAAGAGCGGTTTAAATCTTAAATAAAGCGCT	2267
2535	Qy	CTTTTTATAGAAAAAATTCCTTTAGCGTGGTTTTTTTCGAAATGCTGGCGGTACCCAGA	2594
2268	Db	CTTTTTATAGAAAAAATTCCTTTAGCGTGGTTTTTTTCGAAATGCTGGCGGTACCCAGA	2327
2595	Qy	ATTAGAAATCAGTAGATCAAAATTTATCACGAATAGAAATCAGGAAAAATCAGATCCAAACAT	2654
2328	Db	ATTAGAAATCAGTAGATCAAAATTTATCACGAATAGAAATCAGGAAAAATCAGATCCAAACAT	2387
2655	Qy	AAAAACACTAGAACAAATTCGAAAGTTTAACTACTCAACGCTAGTAGTGGAATTTAATCCC	2714
2388	Db	AAAAACACTAGAACAAATTCGAAAGTTTAACTACTCAACGCTAGTAGTGGAATTTAATCCC	2447

QY	2715	AAATGAGCCAAACAGAACAGAGCCAGAGAAACAGAAATCAGAA	CAAGTAAACATGGAATTTAGA	2774
DB	2448	AAATGAGCCAAACAGAACAGAGCCAGAGAAACAGAAATCAGAA	CAAGTAAACATGGAATTTAGA	2507
QY	2775	AATCGAAGAGAAAGAAAGCAATGACTCGTGTGAAATAATGC	CACGAATCGTTCCTTATTT	2834
DB	2508	AATCGAAGAGAAAGAAAGCAATGACTCGTGTGAAATAATGC	CACGAATCGTTCCTTATTT	2567
QY	2835	TTTTTTTAAAGCGGTATACCTAGATATAACGAAACACAGAA	CTGAATAGAAACGAAAAAAG	2894
DB	2568	TTTTTTTAAAGCGGTATACCTAGATATAACGAAACACAGAA	CTGAATAGAAACGAAAAAAG	2627
QY	2895	AGCCATGACACATTTATAAATGTTTGCACACATTTTATAAAT	TGCATAGCCCATTAAGAT	2954
DB	2628	AGCCATGACACATTTATAAATGTTTGCACACATTTTATAAAT	TGCATAGCCCATTAAGAT	2687
QY	2955	TGCCAAACCAACGCTTATCAGTTAGTCAGATGAATCTTCCCT	CGTAAGAAGTTATTTAA	3014
DB	2688	TGCCAAACCAACGCTTATCAGTTAGTCAGATGAATCTTCCCT	CGTAAGAAGTTATTTAA	2747
QY	3015	TTAACTTTGTTTGAAGACGGTATATAACCGTACTATCATAT	TATATAGGGAATCAGAGAT	3074
DB	2748	TTAACTTTGTTTGAAGACGGTATATAACCGTACTATCATAT	TATATAGGGAATCAGAGAT	2807
QY	3075	TTTTCAAGTACTAAGCTACTGAATTTAAAGAAATGTTAAAG	CAATCGAAATCGTTTG	3134
DB	2808	TTTTCAAGTACTAAGCTACTGAATTTAAAGAAATGTTAAAG	CAATCGAAATCGTTTG	2867
QY	3135	ATTGCTTTTTTGTATTCAATTTATAGAAGTGGAGTTTGTAT	GAATCATGATGAATGTAA	3194
DB	2868	ATTGCTTTTTTGTATTCAATTTATAGAAGTGGAGTTTGTAT	GAATCATGATGAATGTAA	2927
QY	3195	AACCTTATATAAATAAGTTTATGAGATAGAABAATTAGCRA	ANTATCTATACACTAGA	3254
DB	2928	AACCTTATATAAATAAGTTTATGAGATAGAABAATTAGCRA	ANTATCTATACACTAGA	2987
QY	3255	AACGTTTAAAGAAAGAGTTAGAAAAGAGAAATATCTACT	TTAGAAACAAAATCAGATAAGTA	3314
DB	2988	AACGTTTAAAGAAAGAGTTAGAAAAGAGAAATATCTACT	TTAGAAACAAAATCAGATAAGTA	3047
QY	3315	TTTTTCTTCGAGGGGGAAGATTTATATAATAGTTTAAATAG	AAAATAACAAAATATTTA	3374
DB	3048	TTTTTCTTCGAGGGGGAAGATTTATATAATAGTTTAAATAG	AAAATAACAAAATATTTA	3107
QY	3375	TTGATTTAGTGGAAAAAATTTGACTTATATAAGGAAAAAAT	CTTTTTTCAAAAATCATGCAAT	3434
DB	3108	TTGATTTAGTGGAAAAAATTTGACTTATATAAGGAAAAAAT	CTTTTTTCAAAAATCATGCAAT	3167
QY	3435	ATTGAACAGTTGAAATGAAAGAAACCAAGTTTATAACACCT	ATAATTTTATAGGATT	3494
DB	3168	ATTGAACAGTTGAAATGAAAGAAACCAAGTTTATAACACCT	ATAATTTTATAGGATT	3227
QY	3495	TATAGGAAAGGAGAACAGCTGAATGAATATCCCTTTGTTGT	AGAACTGTGCTTCATGA	3554
DB	3228	TATAGGAAAGGAGAACAGCTGAATGAATATCCCTTTGTTGT	AGAACTGTGCTTCATGA	3287
QY	3555	CGGCTTGTAAAGTACAAATTTAAAAATAGTAAAAATTCGCT	CAATCATACCAAGCCAGG	3614
DB	3288	CGGCTTGTAAAGTACAAATTTAAAAATAGTAAAAATTCGCT	CAATCATACCAAGCCAGG	3347
QY	3615	TAAAGCAAGAGGGGCTATTTTTTCGGTATCGCTCAAAATCA	AGCATGATTCGGGGTCTGCG	3674
DB	3348	TAAAGCAAGAGGGGCTATTTTTTCGGTATCGCTCAAAATCA	AGCATGATTCGGGGTCTGCG	3407
QY	3675	TGTTGTTCTGACCTTCGAGGAAGCGATTCGAAGAAATCAAG	ATATACATTTACATTTGGAC	3734
DB	3408	TGTTGTTCTGACCTTCGAGGAAGCGATTCGAAGAAATCAAG	ATATACATTTACATTTGGAC	3467
QY	3735	ACCCAAAGTTTATCGTTATCGACAGTATCGACAGGAAACCG	TTTCATACACGAAAGGACA	3794
DB	3468	ACCCAAAGTTTATCGTTATCGACAGTATCGACAGGAAACCG	TTTCATACACGAAAGGACA	3527

4608	QY	AGAAAGCTATATAAAGGGCGCTGACAAATTCCTTTGACTTTAGAGCATACATTCATTCAAGA	4667
4935	QY	GACTTTAAACAAAGCTAGCAGAAACGCCCTAAACCGGACACACAATCGATTCGATTTTAGCTA	4994
4668	Db	GACTTTAAACAAAGCTAGCAGAAACGCCCTAAACCGGACACACAATCGATTCGATTTTAGCTA	4727
4995	QY	TGATACAGCTGAAATTAATAACCCGCACTATGCCAATACATTTATCTATGATACGCTGT	5054
4728	Db	TGATACAGCTGAAATTAATAACCCGCACTATGCCAATACATTTATCTATGATACGCTGT	4787
5055	QY	TTGTTTTTCTTTGCTGTTTTAGCGAATGATTAGCAGAAATATACAGAGTAAGATTTTAAT	5114
4788	Db	TTGTTTTTCTTTGCTGTTTTAGCGAATGATTAGCAGAAATATACAGAGTAAGATTTTAAT	4847
5115	QY	TAAATTATTAGGGGGAGAGGAGAGTAGTACCCGAAACTTTTAGTTGCTTGGACTGAC	5174
4848	Db	TAAATTATTAGGGGGAGAGGAGAGTAGTACCCGAAACTTTTAGTTGCTTGGACTGAC	4907
5175	QY	GAAGTCAGGGAAAGGCTACTTAAACCGTCGAGGGCAGTCAGAGCGAAACGCACTTGT	5234
4908	Db	GAAGTCAGGGAAAGGCTACTTAAACCGTCGAGGGCAGTCAGAGCGAAACGCACTTGT	4967
5235	QY	TTTTTAAATTTTCTATCTTTTATAGTCAATAGAGTATACTTATTTTGTCTTATTAACATT	5294
4968	Db	TTTTTAAATTTTCTATCTTTTATAGTCAATAGAGTATACTTATTTTGTCTTATTAACATT	5027
5295	QY	TAGCAGCATAAATAGATTTTATCGAATAGTCACTTTAAGTTGACATATTAGAGGAGAAAA	5354
5028	Db	TAGCAGCATAAATAGATTTTATCGAATAGTCACTTTAAGTTGACATATTAGAGGAGAAAA	5087
5355	QY	TCTTCGAGAAATATTTTGAAGAACCCGATTACATGATTCGATTAGTTCTTTGGTTCAGT	5414
5088	Db	TCTTCGAGAAATATTTTGAAGAACCCGATTACATGATTCGATTAGTTCTTTGGTTCAGT	5147
5415	QY	GGTTTTTAACTAAAAGTAGTGAATTTTTGATTTTTGGTGTGTGTCTTTGTTGTTAGTAT	5474
5148	Db	GGTTTTTAACTAAAAGTAGTGAATTTTTGATTTTTGGTGTGTGTCTTTGTTGTTAGTAT	5207
5475	QY	TTGCTAGTCAAAAGTGATTTAAATA	5497
5208	Db	TTGCTAGTCAAAAGTGATTTAAATA	5230

RESULT 5
US-09-070-927A-287/c
; Sequence 287, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunsch
; Patrick J. Dillon
; Steven Barash
; TITLE OF INVENTION: Enterococcus faecalis polynucleotides and polypeptides

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US-09-070-927A-287/c
; Sequence 287, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
;
; APPLICANT: Charles A. Kunsch
;           Patrick J. Dillon
;           Steven Barash
;
; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
;
; NUMBER OF SEQUENCES: 982
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Human Genome Sciences, Inc.
;   STREET: 9410 Key West Avenue
;   CITY: Rockville
;   STATE: Maryland
;   COUNTRY: USA
;   ZIP: 20850
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;   COMPUTER: HP Vectra 486/33
;   OPERATING SYSTEM: MEDOS version 6.2
;   SOFTWARE: ASCII Text
;
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/070,927A
;   FILING DATE: 04-May-2000
;   CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 60/046,655
;   FILING DATE: 1997-05-16

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APPLICATION NUMBER: 60/044,031
 FILING DATE: 1997-05-06
 APPLICATION NUMBER: 60/066,009
 FILING DATE: 1997-11-14
 ATTORNEY/AGENT INFORMATION:
 NAME: Kenley K. Hoover
 REGISTRATION NUMBER: 40,302
 REFERENCE/DOCKET NUMBER: PB369
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ ID NO: 287:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3765 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 287:
 US-09-070-927A-287

Query Match 26.1%; Score 1434.8; DB 9; Length 3765;

Best Local Similarity 96.6%; Pred. No. 3.4e-270; Indels 2; Gaps 2;
 Matches 1485; Conservative 2; Mismatches 49;

QY	3488	TAGGATTTATAGGAAGAGAACAGCTGAATGAATATCCCTTTTGGTTGTAGAACTGTGC	3547
DB	2075	TAATTTTCGTAAGAAGAGAACAGCTGAATGAATATCCCTTTTGGTTGTAGAACTGTGC	2016
QY	3548	TTCATGACGGCTGTTAAAGTACAAATTTAAATAAGTAAATTCGCTCAATCACTACCA	3607
DB	2015	TTCATGACGGCTGTTAAAGTACAAATTTAAATAAGTAAATTCGCTCAATCACTACCA	1956
QY	3608	AGCCAGGTAAAGCAAGAGGGCTATTTTGGTATCGCTCAAAATCAAGCATGATGGCG	3667
DB	1955	AGCCAGGTAAAGCAAGAGGGCTATTTTGGTATCGCTCAAAATAAGCATGATGGCG	1896
QY	3668	GTCGTGGTGTGTTCTGACTTCCGAGGAGCGATTCAGAAATCAAGATACATTTACAC	3727
DB	1895	GACGTGGGTGTTCTGACTTCCGAGGAGCGATTCAGAAATCAAGATACATTTACGC	1836
QY	3728	ATTGACACCCAAAGTATTATCGTTATGGAAGTATGACGAGCAAAACCGTTTCATACGA	3787
DB	1835	ATTGACACCCAAAGTATTATCGTTATGGAAGTATGACGAGCAAAACCGTTTCATACGA	1776
QY	3788	AAGGACATTCGAAACAAATTTAAGACAAATCAATACCTTTCTTTATGATTTTGATATTC	3847
DB	1775	AAGGACATTCGAAACAAATTTAAGACAAATCAATACCTTTCTTTATGATTTTGATATTC	1716
QY	3848	ACAGGCAAAAGAACTATTTTCAGCAAGCGATATTTTAAACAACCGCTATTGATTAGGTT	3907
DB	1715	ACAGGCAAAAGAACTATTTTCAGCAAGCGATATTTTAAACAACCGCTATTGATTAGGTT	1656
QY	3908	TTATGCTTACTATGATATCAATCTGATAAGGTTATCAAGCATATTTTGTGTTTAGAAA	3967
DB	1655	TTATGCTTACTATGATATCAATCTGATAAGGTTATCAAGCATATTTTGTGTTTAGAAA	1596
QY	3968	CGCAGTCTATGACTTCAAAATCAGAAATTAATCTGTCAGAGCGCAAAATATTTT	4027
DB	1595	CGCCAGT-TATGTGACTTCAAAATCAGAAATTAATCTGTCAGAGCGCAAAATATTTT	1538
QY	4028	CGCAAAATATCCGAGATATTTTGGAAAGTCTTTGCCAGTTGATCTAACGTGTAATCAT	4087
DB	1537	CGCAAAATATCCGAGATATTTTGGAAAGTCTTTGCCAGTTGATCTAACGTGTAATCAT	1478
QY	4088	TTGATATTCGCGATACCAAGAACGCAATATGATAGAAATTTTGTATTCCTTAATACCGTT	4147
DB	1477	TTGGAAWTGCTCGTATACCAAGAACGCAATATGATAGAAATTTTGTATTCCTTAATACCGTT	1418
QY	4148	ATTCCTTTCAAGAAATGGCAAGATTTGCTTTTCAAAACAAACAGATATTAAGGCTTTACTC	4207
DB	1417	ATTCCTTTCAAGAAATGGCAAGATTTGCTTTTCAAAACAAACAGATATTAAGGCTTTACTC	1358
QY	4208	GTTCAAGTCTAACGGTTTAAAGCGGTACAGAGGCAAAATAAGTATGAAACCCCTGGT	4267

DB	1357	GTTCAAGTCTAACGGTTTAAAGCGGTACAGAGGCAAAATAAGTAGTGAACCCCTGGT	1298
QY	4268	TTAATCTCTTATTGCACGAAACGAAATTTTCAGGAGAAAGGGTTTAAATAGGCGGTATA	4327
DB	1297	TTAATCTCTTATTGCACGAAACGAAATTTTCAGGAGAAAGGGTTTAAATAGGCGGTATA	1238
QY	4328	ACGTCAATGTTTACCTCTCTTTTAGCCTACTTTTAGTTTCAAGTATTCATTCGAAAGCTGCG	4387
DB	1237	ACGTCAATGTTTACCTCTCTTTTAGCCTACTTTTAGTTTCAAGTATTCATTCGAAAGCTGCG	1178
QY	4388	AATATAATATGTTTTCAGTTTAAATATCGATTAGATCAACCTTTAGAGAAAGAAAGTAA	4447
DB	1177	AATATAATATGTTTTCAGTTTAAATATCGATTAGATCAACCTTTAGAGAAAGAAAGTAA	1118
QY	4448	TCAAAATGTTTAGAAGTGCCTTATTCAGAAACTATCAAGGGGCTTAATAGGGAATACATTA	4507
DB	1117	TTAAACTTGTTAGAAGTGCCTTATTCAGAAACTATCAAGGGGCTTAATAGGGAATACATTA	1058
QY	4508	CCATCTCTTTCGAAAGCTTGGGTATCAAGTATTAACCTTAACAGTAAAGATTTTGTCCGTC	4567
DB	1057	CCATCTCTTTCGAAAGCTTGGGTATCAAGTATTAACCTTAACAGTAAAGATTTTGTCCGTC	998
QY	4568	AAGGCTGGTTTAAATTCAGAAAGAAAGAGCGAACGTCACGTTTCATTTGTCAGAAAT	4627
DB	997	AAGGCTGGTTTAAATTCAGAAAGAAAGAGAGCGAACGTCACGTTTCATTTGTCAGAAAT	938
QY	4628	CGAAAGAGATTTAATGCTTATATTCGGAAGAAAGCGATGTATACAGGCTTATTAG	4687
DB	937	CGAAAGAGATTTAATGCTTATATTCGGAAGAAAGCGATGTATACAGGCTTATTAG	878
QY	4688	TCACCAACCAAAAGAGATTTAGAGAGTGTAGGCAATTCCTGAAACGGACATTAGATAAT	4747
DB	877	TCACCAACCAAAAGAGATTTAGAGAGTGTAGGCAATTCCTGAAACGGACATTAGATAAT	818
QY	4748	TGCTGAAAGTACTGAAGCGGAATCAGGAAATTTCTTTAAGATTAACCCAGAGAAATG	4807
DB	817	TGCTGAAAGTACTGAAGCGGAATCAGGAAATTTCTTTAAGATTAACCCAGAGAAATG	758
QY	4808	GTGGCAATTCACCTCTGATGTTTAAATCATTTGCTATCGATCATTTAAAGTAAAAAAG	4867
DB	757	GTGGCAATTCACCTCTGATGTTTAAATCATTTGCTATCGATCATTTAAAGTAAAAAAG	698
QY	4868	AAGAAAAAGAAAGCTATATAAGCGCTGACAAATTTCTTTGACTTAGAGGATACATTC	4927
DB	697	AAGAAAAAGAAAGCTATATAAGCGCTGACAAATTTCTTTGACTTAGAGGATACATTC	638
QY	4928	TTTCAAGAGCTTTTAAACAGCTAGCAGAACCCCTTAAACCGGACACACCACTTCGATTTGT	4987
DB	637	TTTCAAGAGCTTTTAAACAGCTAGCAGAACCCCTTAAACCGGACACACCACTTCGATTTGT	578
QY	4988	TTAGCTATGATACAGGCTGAAATTAACCCCGCACTAT 5025	
DB	577	TTAGCTATGATACAGGCTGAAATTAAGTCCGCTAT 540	

RESULT 6

US-10-032-393-7/c
 ; Sequence 7, Application US/10032393
 ; Publication No. US20030027286A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Gross, Molly
 ; TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
 ; FILE REFERENCE: ELITRA.010A
 ; CURRENT APPLICATION NUMBER: US/10/032.393
 ; CURRENT FILING DATE: 2001-12-21
 ; PRIOR APPLICATION NUMBER: 60/259,434
 ; PRIOR FILING DATE: 2000-12-27
 ; PRIOR APPLICATION NUMBER: 09/948,993
 ; PRIOR FILING DATE: 2001-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,335

;; PRIOR FILING DATE: 2000-09-06
;; NUMBER OF SEQ ID NOS: 68
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 7
;; LENGTH: 10929
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Vector pEP25
US-10-032-393-7

Query Match 20.2%; Score 1109.4; DB 15; Length 10929;
Best Local Similarity 99.9%; Pred. No. 2.8e-206;
Matches 1110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 936 AAAAGAAAAACGAAATGATACACCAATCAGTGCAGAAAAAAGATATATATGGGAGATAAGAC 995
DB 5830 AAAAGAAAAACGAAATGATACACCAATCAGTGCAGAAAAAAGATATATATGGGAGATAAGAC 5771

QY 996 GGTTCGTGTCGTGCTGACTTGACCATATATCAATAAATCGAAACAGCAAGAAATGGCGG 1055
DB 5770 GGTTCGTGTCGTGCTGACTTGACCATATATCAATAAATCGAAACAGCAAGAAATGGCGG 5711

QY 1056 AAAACGTAAAGAAAGTATGGAATAAGACTTAGAAGCAAACTTAAAGAGTGTGTGATAGT 1115
DB 5710 AAACGTAAAGAAAGTATGGAATAAGACTTAGAAGCAAACTTAAAGAGTGTGTGATAGT 5651

QY 1116 GCAGTATCTTAAATTTGTATTAATAGGAATGGAAGTAAATAGATGCTAAATTTGT 1175
DB 5650 GCAGTATCTTAAATTTGTATTAATAGGAATGGAAGTAAATAGATGCTAAATTTGT 5591

QY 1176 AATTAGAGAGGAGTGTATCATCAACAAATAATAAATATCTCAAACTTTTAAACGA 1235
DB 5590 AATTAGAGAGGAGTGTATCATCAACAAATAATAAATATCTCAAACTTTTAAACGA 5531

QY 1236 GTGAAAAAGTACTCAACCAATATATAAACAATTTGAATTTAAAGAAACCGATACCGTTT 1295
DB 5530 GTGAAAAAGTACTCAACCAATATATAAACAATTTGAATTTAAAGAAACCGATACCGTTT 5471

QY 1296 ACCAAATTTGGAACAGGTAAAGGCAATTAACGACGAATCTGCTAAATTAAGTAAACAGG 1355
DB 5470 ACCAAATTTGGAACAGGTAAAGGCAATTAACGACGAATCTGCTAAATTAAGTAAACAGG 5411

QY 1356 TAAAGTCTATTTGAATTTAGACAGTCACTTATCAACTTATCGTCAGAAAAATTAACACTGA 1415
DB 5410 TAAAGTCTATTTGAATTTAGACAGTCACTTATCAACTTATCGTCAGAAAAATTAACACTGA 5351

QY 1416 ATACTCGTGTCACTTTAATTCACCAAGATATCTCAGTTTCAATTCCTTAACAAACAGA 1475
DB 5350 ATACTCGTGTCACTTTAATTCACCAAGATATCTCAGTTTCAATTCCTTAACAAACAGA 5291

QY 1476 GGTATAAAAATTTGTGGAGTATTCCTTACCATTTAAGACACAAATTTATTAAGAAAGTGG 1535
DB 5290 GGTATAAAAATTTGTGGAGTATTCCTTACCATTTAAGACACAAATTTATTAAGAAAGTGG 5231

QY 1536 TTTTGAAGCCATGCGTCTGACATCTATCTGATTTGGAAGAGGATTTCTAAGCGGTA 1595
DB 5230 TTTTGAAGCCATGCGTCTGACATCTATCTGATTTGGAAGAGGATTTCTAAGCGGTA 5171

QY 1596 CTTTGGATATTCACCGAACACTAGGCTGCTCTTTCACACTCAAGTCTCGATTCAGCAT 1655
DB 5170 CTTTGGATATTCACCGAACACTAGGCTGCTCTTTCACACTCAAGTCTCGATTCAGCAT 5111

QY 1656 TGCTTAAGCTGCCAGGGGAATGCTTTTCATCTCAACCAAAAGTAAACAGTGTCTTAATAA 1715
DB 5110 TGCTTAAGCTGCCAGGGGAATGCTTTTCATCTCAACCAAAAGTAAACAGTGTCTTAATAA 5051

QY 1716 AACTTACCGCCATACACAGATGTTCCAGATTAATTTGGAAGCTATATAGTACTTTG 1775
DB 5050 AACTTACCGCCATACACAGATGTTCCAGATTAATTTGGAAGCTATATAGTACTTTG 4991

QY 1776 TTTCAAAATGGGTCATTCAGATAATCGTCAACTGTTTACTAAAAATCAGTTTCATCAAG 1835

DB 4990 TTTCAAAATGGTCAATCGAGATATCGTCAACTGTTTACTAAAAATCAGTTTCATCAAG 4931
QY 1836 CAATGAAACACGCCAAAGTAAACAATTTAAGTACCGTTTACTTATGACCAAGTATTGTCTA 1895
DB 4930 CAATGAAACACGCCAAAGTAAACAATTTAAGTACCGTTTACTTATGACCAAGTATTGTCTA 4871
QY 1896 TTTTAAATAGTATCTATTTAATTAACCGGAGAGAAATATTTCTATGAGTCGCTTTTGTAAA 1955
DB 4870 TTTTAAATAGTATCTATTTAATTAACCGGAGAGAAATATTTCTATGAGTCGCTTTTGTAAA 4811
QY 1956 TTTGAAAGTTACACGTTTACTTAAAGGAATCGTAGATAAATTTATAGGTATATACTACTGACA 2015
DB 4810 TTTGAAAGTTACACGTTTACTTAAAGGAATCGTAGATAAATTTATAGGTATATACTACTGACA 4751
QY 2016 GTTCCAAAGAGCTAAAGAGGTCCTAGCGC 2046
DB 4750 GTTCCAAAGAGCTAAAGAGGTCCTAGCGC 4720

RESULT 7
US-10-032-393-51/c
; Sequence 51, Application US/10032393
; Publication No. US20030027286A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Wall, Daniel
; APPLICANT: Gross, Molly
; TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
; FILE REFERENCE: ELITRA.010A
; CURRENT APPLICATION NUMBER: US/10/032.393
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/259,434
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 09/948,993
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 9412
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pEP25
US-10-032-393-51

Query Match 15.9%; Score 876.6; DB 15; Length 9412;
Best Local Similarity 83.4%; Pred. No. 9e-161;
Matches 1102; Conservative 0; Mismatches 9; Indels 210; Gaps 1;

QY 936 AAAAGAAAAACGAAATGATACACCAATCAGTGCAGAAAAAAGATATATATGGGAGATAAGAC 995
DB 6703 AAAAGAAAAACGAAATGATACACCAATCAGTGCAGAAAAAAGATATATATGGGAGATAAGAC 6644

QY 996 GGTTCGTGTCGTGCTGACTTGACCATATATCAATAAATCGAAACAGCAAGAAATGGCGG 1055
DB 6643 GGTTCGTGTCGTGCTGACTTGACCATATATCAATAAATCGAAACAGCAAGAAATGGCGG 6584

QY 1056 AAAAGTAAAGAAAGTATGGAATAAGACTTAGAAGCAAACTTAAAGAGTGTGTGATAGT 1115
DB 6583 AAAAGTAAAGAAAGTATGGAATAAGACTTAGAAGCAAACTTAAAGAGTGTGTGATAGT 6524

QY 1116 GCAGTATCTTAAATTTGTATTAATAGGAATTTAAATTTAGATGCTTAAATTTGT 1175
DB 6523 GCATTTCTTAAATTTGTATTAATAGGAATTTAAATTTAGATGCTTAAATTTGT 6464

QY 1176 AATTAAAG----- 1183
DB 6463 AATTAAAGAGGAGGATTCGTCATGTTGGTATTCCTCAATCGTAAATGTAGATAAACAATC 6404

QY 1184 ----- 1183

QY 1386 TCAACTTATCGTCAGAAAATTAACACTGAATCTCGTGTCACTTTAAATTCACCAAGATA 1445
Db 6043 TCAACTTATCGTCAGAAAATTAACACTGAATCTCGTGTCACTTTAAATTCACCAAGATA 5984
QY 1446 TTCTACAGTTTCAATTCCTTAACAAACACAGAGGTATTAATTTGTTGGAGTATTCCTTACC 1505
Db 5983 TTCTACAGTTTCAATTCCTTAACAAACACAGAGGTATTAATTTGTTGGAGTATTCCTTACC 5924
QY 1506 ATTTAAGCACACAAATTTAAATAAGTGTGTTTGAAGCCATGCGTCTGACATCTATC 1565
Db 5923 ATTTAAGCACACAAATTTAAATAAGTGTGTTTGAAGCCATGCGTCTGACATCTATC 5864
QY 1566 TGATTGTTGAAGAGGATTCACAGGCTACCTTGGATATTCACCGAACAACAGAGGTGTC 1625
Db 5863 TGATTGTTGAAGAGGATTCACAGGCTACCTTGGATATTCACCGAACAACAGAGGTGTC 5804
QY 1626 TCTTGACACTCAAGTCTCGATTTCAGCAATTTGCTTAAGCTGCGAGCGGAATGCTTTCATC 1685
Db 5803 TCTTGACACTCAAGTCTCGATTTCAGCAATTTGCTTAAGCTGCGAGCGGAATGCTTTCATC 5744
QY 1686 CTAACCCAAAGTAACAGTGTCTTAATAAATCTTACCCGCCATACACAGATGTTCCAG 1745
Db 5743 CTAACCCAAAGTAACAGTGTCTTAATAAATCTTACCCGCCATACACAGATGTTCCAG 5684
QY 1746 ATAAATATTCGAAGCTATATACGTACTTCTTTCAAAATGGGTCAATTCAGAAATATCGTC 1805
Db 5683 ATAAATATTCGAAGCTATATACGTACTTCTTTCAAAATGGGTCAATTCAGAAATATCGTC 5624
QY 1806 AACTGTTTACTAAATCAGTTTCATCAGCAATGAACACGCCAAGTAACAAATTTAA 1865
Db 5623 AACTGTTTACTAAATCAGTTTCATCAGCAATGAACACGCCAAGTAACAAATTTAA 5564
QY 1866 GTACCGTACTTATGAGCAAGTATGCTATTTTAAATAGTATCTATTATTAAACGGGA 1925
Db 5563 GTACCGTACTTATGAGCAAGTATGCTATTTTAAATAGTATCTATTATTAAACGGGA 5504
QY 1926 GGAATAATTCATGAGTGCCTTTTGTAAATTTGAAAGTTACAGTTTACTAAAGGAAT 1985
Db 5503 GGAATAATTCATGAGTGCCTTTTGTAAATTTGAAAGTTACAGTTTACTAAAGGAAT 5444
QY 1986 GTAGATAAATTTAGTATCTACTGACAGCTTCCAGGGCTAAGAGGTCCCTTAGCG 2045
Db 5443 GGAGATAAATTTAGTATCTACTGACAGCTTCCAGGGCTAAGAGGTCCCTTAGCG 5384
QY 2046 C 2046
Db 5383 C 5383

RESULT 9
US-10-032-393-48/c
; Sequence 48, Application US/10032393
; Publication No. US20030027286A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Wall, Daniel
; APPLICANT: Gross, Molly
; TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
; FILE REFERENCE: ELITFA.010A
; CURRENT APPLICATION NUMBER: US/10/032,393
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/259,434
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 09/948,993
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 9417
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Vector pPEPER14*
US-10-032-393-48

Query Match 15.9%; Score 876.6; DB 15; Length 9417;
Best Local Similarity 83.4%; Pred. No. 9e-161;
Matches 1102; Conservative 0; Mismatches 9; Indels 210; Gaps 1;
QY 936 AAAAGAAAACGAAATGATACACCAATCAGTCGCAAAAAAGATATAATGGGAGATAAGAC 995
Db 6703 AAAAGAAAACGAAATGATACACCAATCAGTCGCAAAAAAGATATAATGGGAGATAAGAC 6644
QY 996 GGTTCGTGTTCTGTCGTGCTGACCTTGCACCATATCATATAAATCGAAACAGCAAAATCGCGG 1055
Db 6643 GGTTCGTGTTCTGTCGTGCTGACCTTGCACCATATCATATAAATCGAAACAGCAAAATCGCGG 6584
QY 1056 AAACGTAAAGAAGTTATGGAATTAAGACTTAGAAGCAAACTTAAGAGTGTGTTGATAGT 1115
Db 6583 AAACGTAAAGAAGTTATGGAATTAAGACTTAGAAGCAAACTTAAGAGTGTGTTGATAGT 6524
QY 1116 GCAGTATCTTAAATTTTGTATATAAGGAATTAAGTTAAATTTAGATGCTTAAATTTGT 1175
Db 6523 GCATTTATCTTAAATTTTGTATATAAGGAATTAAGTTAAATTTAGATGCTTAAATTTGT 6464
QY 1176 AATTAAAGA----- 1183
Db 6463 AATTAAAGAAGGAGGATTCTGTCATGTTGGTATTCCAATGCGTAAATGTAGATAAAACATC 6404
QY 1184----- 1183
Db 6403 TACTGTTTGAACACAGACTAAAAACAGTATTACGCAGATAATAATAATACGTAGATTAA 6344
QY 1184----- 1183
Db 6343 TTCCTACAGTGACTAATCTTATGACTTTTAAACAGATAACTAAATTAACAACAAATC 6284
QY 1184----- 1205
Db 6283 GTTTAACTTCTGTTTGTGTTTATAGTGTATCACTTCAGGAGAGATTACATGAACAAA 6224
QY 1206 ATATAAATATTTCTCAAACTTTTAAAGAGTGAAGAAAGTACTCAACCAATTAATAAAC 1265
Db 6223 ATATAAATATTTCTCAAACTTTTAAAGAGTGAAGAAAGTACTCAACCAATTAATAAAC 6164
QY 1266 AATTGAATTTAAAGAAACCGATACCCGTTTACGAAATTTGAAACAGGTAAAGGGCATTTAA 1325
Db 6163 AATTGAATTTAAAGAAACCGATACCCGTTTACGAAATTTGAAACAGGTAAAGGGCATTTAA 6104
QY 1326 CGACAAACCTGGCTAAATAAGTAAACAGGTAAACAGTCTATTGAAATTAGACAGTCACTAT 1385
Db 6103 CGACAAACCTGGCTAAATAAGTAAACAGGTAAACAGTCTATTGAAATTAGACAGTCACTAT 6044
QY 1386 TCAACTTATCGTCAGAAAATTTAAACTGTAATCTCGTGTGACCTTTTAAATTCACCAAGATA 1445
Db 6043 TCAACTTATCGTCAGAAAATTTAAACTGTAATCTCGTGTGACCTTTTAAATTCACCAAGATA 5984
QY 1446 TTCTACAGTTTCAATTCCTTAACAAACAGAGGTATAAATTTGTTGGAGTATTCCTTACC 1505
Db 5983 TTCTACAGTTTCAATTCCTTAACAAACAGAGGTATAAATTTGTTGGAGTATTCCTTACC 5924
QY 1506 ATTTAAGCACACAAATTTAAATAAGTGTGTTTGAAGCCATGCGTCTGACATCTATC 1565
Db 5923 ATTTAAGCACACAAATTTAAATAAGTGTGTTTGAAGCCATGCGTCTGACATCTATC 5864
QY 1566 TGATTGTTGAAGAGGATTCACAGGCTACCTTGGATATTCACCGAACAACAGAGGTGTC 1625
Db 5863 TGATTGTTGAAGAGGATTCACAGGCTACCTTGGATATTCACCGAACAACAGAGGTGTC 5804
QY 1626 TCTTGCACTCAAGTCTCGATTTCAGCAATTTGCTTAAGCTGCGAGCGGAATGCTTTCATC 1685
Db 5803 TCTTGCACTCAAGTCTCGATTTCAGCAATTTGCTTAAGCTGCGAGCGGAATGCTTTCATC 5744

Qy	1386	TCAACTTATCGTCAGAAAAATTAAACTGAACTACGTCGTCTCACTTTAAATTCACCAAGATA	1445
Db	11409	TCAACTTATCGTCAGAAAAATTAAACTGAACTACGTCGTCTCACTTTAAATTCACCAAGATA	11350
Qy	1446	TTCTACAGTTTCAATTCCTCAACAAACAGAGGTATAAAAATTGTTGGAGTATTCCTTACC	1505
Db	11349	TTCTACAGTTTCAATTCCTCAACAAACAGAGGTATAAAAATTGTTGGAGTATTCCTTACC	11290
Qy	1506	ATTTAAGCACACAAATATTATAAAAAAGTGGTTTTGAAAGCCATGCGTCTGACATCTATC	1565
Db	11289	ATTTAAGCACACAAATATTATAAAAAAGTGGTTTTGAAAGCCATGCGTCTGACATCTATC	11230
Qy	1566	TGATTCGTTGAAGAGGATTCTCAACGGTACCTTGGATATTACCGAACACTAGGTTGC	1625
Db	11229	TGATTCGTTGAAGAGGATTCTCAACGGTACCTTGGATATTACCGAACACTAGGTTGC	11170
Qy	1626	TCCTGCACACTCAAGTCTCGAATTCAGCAATGCTTAAAGTGCAGCGGAATGCTTTCATC	1685
Db	11169	TCCTGCACACTCAAGTCTCGAATTCAGCAATGCTTAAAGTGCAGCGGAATGCTTTCATC	11110
Qy	1686	CTAAACCAAAGTAAACAGTGTCTTAATAAACTTACCGCCATACACAGATGTTCCAG	1745
Db	11109	CTAAACCAAAGTAAACAGTGTCTTAATAAACTTACCGCCATACACAGATGTTCCAG	11050
Qy	1746	ATAAATATTGGAAGCTATATACGTACTTTGTTTCAAAAATGGGTCAATCGAGAATATCGTC	1805
Db	11049	ATAAATATTGGAAGCTATATACGTACTTTGTTTCAAAAATGGGTCAATCGAGAATATCGTC	10990
Qy	1806	AACGTGTTTACTAAAAATCAGTTTTCATCAAGCAATGAACACGCCAAAGTAAACAATTTAA	1865
Db	10989	AACGTGTTTACTAAAAATCAGTTTTCATCAAGCAATGAACACGCCAAAGTAAACAATTTAA	10930
Qy	1866	GTACCGTTACTTATGAGCAAGTATGCTATTTTAAATTTAATAGTTATCTATTATTAAACGGA	1925
Db	10929	GTACCAATCTTATGAGCAAGTATGCTATTTTAAATTTAATAGTTATCTATTATTAAACGGA	10870
Qy	1926	GGAAATAAATCTATGAGTCGTTTTGFAAATTTGAAAGTTACACGTTACTAAAGGGAAT	1985
Db	10869	GGAAATAAATCTATGAGTCGTTTTGFAAATTTGAAAGTTACACGTTACTAAAGGGAAT	10810
Qy	1986	GTAGATAAATTTATGATATCTACTGACAGCTTCCAGAGCTAAAGAGTCCCTAGCG	2045
Db	10809	GGAGATAAATTTATGATATCTACTGACAGCTTCCAGAGCTAAAGAGTCCCTAGCG	10750
Qy	2046	C 2046	
Db	10749	C 10749	

Search completed: September 2, 2004, 06:05:50
Job time : 2788 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: September 1, 2004, 14:20:49 ; Search time 12630 Seconds
(without alignments)
12997.023 Million cell updates/sec

Title: US-10-030-390-2
Perfect score: 5497
Sequence: 1 gaattcgattagtcattctt.....ctagtcgaagtattaaata 5497

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:**

- 1: em_estba:**
- 2: em_esthum:**
- 3: em_estin:**
- 4: em_estnu:**
- 5: em_estov:**
- 6: em_estpl:**
- 7: em_estro:**
- 8: em_htc:**
- 9: gb_est1:**
- 10: gb_est2:**
- 11: gb_htc:**
- 12: gb_est3:**
- 13: gb_est4:**
- 14: gb_est5:**
- 15: em_estfun:**
- 16: em_estom:**
- 17: em_gss_hum:**
- 18: em_gss_inv:**
- 19: em_gss_pln:**
- 20: em_gss_vrt:**
- 21: em_gss_fun:**
- 22: em_gss_man:**
- 23: em_gss_mus:**
- 24: em_gss_pro:**
- 25: em_gss_rod:**
- 26: em_gss_pbg:**
- 27: em_gss_vrl:**
- 28: gb_gss1:**
- 29: gb_gss2:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	204	3.7	354	13	BY102466
2	204	3.7	390	9	AI323443
3	204	3.7	451	9	AI893383
4	204	3.7	455	9	AI323089

5	204	3.7	456	9	AA060105
6	204	3.7	456	14	W83072
7	204	3.7	473	13	BY708773
8	204	3.7	474	11	AK008625
9	204	3.7	474	11	AK010179
10	204	3.7	475	11	AK008809
11	204	3.7	477	11	AK008873
12	204	3.7	486	13	BY708705
13	204	3.7	505	13	BY708809
14	204	3.7	505	13	AV072530
15	200.8	3.7	384	13	BY076652
16	200.4	3.6	354	13	BY101861
17	191.2	3.5	311	10	BS564851
18	188	3.4	435	9	AA097254
19	186.4	3.4	311	10	BS564891
20	181.8	3.3	443	14	W12684
21	168.4	3.1	307	10	BS565090
22	166.6	3.0	306	10	BS565053
23	165	3.0	238	29	AY419513
24	160.2	2.9	263	10	BS564847
25	156.4	2.8	332	9	AV076259
26	155	2.8	705	10	BB667664
27	155	2.8	1515	11	AK050258
28	153.8	2.8	300	10	BS564905
29	141	2.6	421	10	BB738530
30	139.4	2.5	1658	28	BH770822
31	138	2.5	354	10	BF707544
32	136.2	2.5	298	10	BS565023
33	135.6	2.5	264	10	BS564882
34	132.8	2.4	242	10	BS565149
35	130.8	2.4	812	12	BM536445
36	130.6	2.4	255	10	BS564787
37	129.8	2.4	602	28	B06973
38	125.8	2.3	254	10	BS565113
39	124.8	2.3	317	9	AV075620
40	122.6	2.2	320	9	AV081837
41	119.8	2.2	304	9	AV075572
42	116.6	2.1	301	9	AV077679
43	116.2	2.1	208	10	BS564887
44	116.2	2.1	308	9	AV080925
45	115.8	2.1	300	9	AV074919

ALIGNMENTS

RESULT 1
BY102466
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

BY102466 354 bp mRNA linear EST 07-DEC-2002
BY102466 RIKEN full-length enriched, pooled tissues, adult spleen,
etc. Mus musculus cDNA clone K630145D13 5', mRNA sequence.
BY102466
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 354)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gofobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
Chothia, C., Corbani, L.E., Cousins, S., Balla, E., Bragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Kongsawa, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Matsuda, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,

FEATURES	Location/Qualifiers	
	source	1..455
FEATURES	Location/Qualifiers	
	source	1..455
MGI:292325		
Putative full length read		
vector to vector length is 457		
Seq primer: -28M13 rev2 from Amersham.		
Location/Qualifiers		
1..455		
/organism="Mus musculus"		
/mol_type="mRNA"		
/db_xref="taxon:10090"		
/clones="IMAGE:481581"		
/dev_stage="19.5 dpc total fetus"		
/lab_host="DH10B (ampicillin resistant)"		
/clone_lib="Soares mouse p3NMF19.5"		
/note="Vector: p773D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Patima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."		
ORIGIN		
Query Match 3.7%; Score 204; DB 9; Length 455;		
Best Local Similarity 100.0%; Pred. NO. 5.6e-26;		
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	296	GCCAGGCCAGGCCAGGCCAGGCCAGGAAACATGTATCATGCGCCCGGGAG 355
DB	73	GCCAGGCCAGGCCAGGCCAGGCCAGGAAACATGTATCATGCGCCCGGGAG 132
QY	356	AGGATAATTGCTTCCCGGTGTACCGCCAGGAGTGCACGGAGAGGTGCTGT 415
DB	133	AGGATAATTGCTTCCCGGTGTACCGCCAGGAGTGCACGGAGAGGTGCTGT 192
QY	416	TTTGATGACAGTGTCCCGGGATTCCCGTGTGCTTCCACCCCATGGCCATCGAAGAACT 475
DB	193	TTTGATGACAGTGTCCCGGGATTCCCGTGTGCTTCCACCCCATGGCCATCGAAGAACT 252
QY	476	CAAGAAGAAGATGTCCTTTCTAA 499
DB	253	CAAGAAGAAGATGTCCTTTCTAA 276
RESULT 5		
AA060105		
LOCUS		
DEFINITION		
mJ7f11.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone		
IMAGE:481581 5', similar to gb:221858 M.Musculus mRNA for P domain		
protein (MOUSE);, mRNA sequence.		
ACCESSION		
AA060105		
VERSION		
AA060105.1 GI:1553793		
KEYWORDS		
EST.		
SOURCE		
Mus musculus (house mouse)		
ORGANISM		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
1 (bases 1 to 456)		
REFERENCE		
AUTHORS		
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.		
TITLE		
The WashU-HMI Mouse EST Project		
JOURNAL		
COMMENT		
Unpublished (1996)		
Contact: Marra M/Mouse EST Project		
WashU-HMI Mouse EST Project		
Washington University School of MedicineP		
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108		
Tel: 314 286 1800		
Fax: 314 286 1810		
Email: mouseest@watson.wustl.edu		
This clone is available royalty-free through LNL; contact the		
IMAGE Consortium (infoimage.llnl.gov) for further information.		
AA060105		
456 bp mRNA linear EST 23-SEP-1996		
mJ7f11.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone		
IMAGE:481581 5', similar to gb:221858 M.Musculus mRNA for P domain		
protein (MOUSE);, mRNA sequence.		
ACCESSION		
AA060105		
VERSION		
AA060105.1 GI:1553793		
KEYWORDS		
EST.		
SOURCE		
Mus musculus (house mouse)		
ORGANISM		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
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AUTHORS		
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JOURNAL		
COMMENT		
Unpublished (1996)		
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WashU-HMI Mouse EST Project		
Washington University School of MedicineP		
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108		
Tel: 314 286 1800		
Fax: 314 286 1810		
Email: mouseest@watson.wustl.edu		
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Tel: 314 286 1800
Fax: 314 286 1810

Email: mousees@watson.wustl.edu

This clone is available royalty-free through LMNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:248318

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 321.

FEATURES

Location/Qualifiers

source

1..456

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:404550"

/dev_stage="19.5 dpc total fetus"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares mouse p3NMF19.5"

/notes="Vector: pT73D (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTT 3']

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT73 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

Soares and M.Fatima Bonaldo. RNA was kindly provided by

Dr. Minoru Ko (Wayne State University)."

ORIGIN

Query Match 3.7%; Score 204; DB 14; Length 456;

Best Local Similarity 100.0%; Pred. No. 5.6e-26;

Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 GCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGAAACATGTATCATGCCCCCGGGAG 355

Db 72 GCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGAAACATGTATCATGCCCCCGGGAG 131

QY 356 AGGATAAATTGGCTTCCCGGTGTACCGCCAGCAGTGACGAGAGAGTGTCTGT 415

Db 132 AGGATAAATTGGCTTCCCGGTGTACCGCCAGCAGTGACGAGAGAGTGTCTGT 191

QY 416 TTGTGATGACAGTGTCCGGGATTCCTGTGTCCACCCATGCCATCAGAACACT 475

Db 192 TTGTGATGACAGTGTCCGGGATTCCTGTGTCCACCCATGCCATCAGAACACT 251

QY 476 CAAGAGAGAGATGTCCCTCTTAA 499

Db 252 CAAGAGAGAGATGTCCCTCTTAA 275

RESULT 7

BY708773

LOCUS BY708773 RIKEN full-length enriched, adult male stomach Mus

DEFINITION musculus cDNA clone 2210409105 5', mRNA sequence.

ACCESSION BY708773

VERSION BY708773.1 GI:271119967

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 473)

AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,

Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,

Kiyosawa,H., Tagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,

Schönbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,

Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,

Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,

Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,

Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,

Cariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,

Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Kongsaya,A.,
Kurochin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Matais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Nunata,K., Okido,T., Pavan,W.J., Perte,G., Pesole,G.,
Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
Sultana,R., Takanaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
Verardo,R., Wagner,L., Wanstedt,C., Wang,Y., Watanabe,Y.,
Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Rogers,J., Birney,E. and Hayashizaki,Y.

Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

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Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,

URL: http://genome.gsc.riken.go.jp/

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,

Fukuda,S., Hashizume,M., Hayashida,K., Hirozane,T., Hori,F.,

Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,

Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,

Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,

Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tegami,M.,

Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

Direct Submission

Computational Analysis of Full-length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in Riken.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for

further details.

Location/Qualifiers

1..473

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="2210409105"

/sex="male"

/tissue_type="stomach"

/dev_stage="adult"

/lab_host="SOLR"

/clone_lib="RIKEN full-length enriched, adult male

stomach"

/note="Site 1: XhoI; Site 2: SstI; cDNA library was

prepared and sequenced in Mouse Genome Encyclopedia

Project of Genome Exploration Research Group in Riken

FEATURES

source

Query Match	3.7%	Score 204;	DB 11;	Length 474;
Best Local Similarity	100.0%;	Pred. No. 5.5e-26;		
Matches 204;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	296	GCACAGGCCACAGGCCACAGGCCACAGGAGAAACATGTATCATGTGCCCCCCCGGAG	355	
Db	91	GCCACAGGCCACAGGCCACAGGCCACAGGAGAAACATGTATCATGTGCCCCCCCGGAG	150	
QY	356	AGGATAAATTGTGGCTTCCCGGTGTACACGCCACAGCAGTGCACGAGAGAGGTTGCTGT	415	
Db	151	AGGATAAATTGTGGCTTCCCGGTGTACACGCCACAGCAGTGCACGAGAGAGGTTGCTGT	210	
QY	416	TTTGATGACAGTGCACGGGATTCCTCGTGGTCTTCCACCCCATGCCCATCGAGAACT	475	
Db	211	TTTGATGACAGTGCACGGGATTCCTCGTGGTCTTCCACCCCATGCCCATCGAGAACT	270	
QY	476	CAAGAAGAAGATGTCCCTTCTAA	499	
Db	271	CAAGAAGAAGATGTCCCTTCTAA	294	

RESULT 10	AK008809	475 bp	mRNA	linear	HTC 20-SEP-2003
LOCUS	Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210403C21	product:trefol factor 1, full insert sequence.			
DEFINITION	AK008809	1	GI:12843228		
ACCESSION	AK008809				
VERSION	HTC; CAP trapper.				
KEYWORDS	Mus musculus (house mouse)				
SOURCE	Mus musculus				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	Carninci, P. and Hayashizaki, Y.				
AUTHORS	High-efficiency full-length cDNA cloning				
TITLE	Mech. Enzymol. 303, 19-44 (1999)				
JOURNAL	9279253				
MEDLINE	10349636				
PUBMED					
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Osawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PUBMED	11076861				
REFERENCE	4				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 585-590 (2001)				
REFERENCE	5				
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.				
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs				
JOURNAL	Nature 420, 563-573 (2002)				
REFERENCE	6				
AUTHORS	(bases 1 to 475)				
TITLE	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ono, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T., Segabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Direct Submission				
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN) Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,				
REFERENCE	7				
AUTHORS	AK008873				
TITLE	LOCUS				
DEFINITION	Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:221049105				
ACCESSION	AK008873				
VERSION	AK008873.1				
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
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AUTHORS	High-efficiency full-length cDNA cloning				
TITLE	Mech. Enzymol. 303, 19-44 (1999)				
JOURNAL	9279253				
MEDLINE	10349636				
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AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Osawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
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JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
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AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 585-590 (2001)				
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AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.				
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs				
JOURNAL	Nature 420, 563-573 (2002)				
REFERENCE	6				
AUTHORS	(bases 1 to 475)				
TITLE	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ono, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T., Segabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Direct Submission				
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN) Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,				
REFERENCE	7				
AUTHORS	AK008873				
TITLE	LOCUS				
DEFINITION	Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:221049105				
ACCESSION	AK008873				
VERSION	AK008873.1				
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
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ACCESSION	AK008873				
VERSION	AK008873.1				
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	Carninci, P. and Hayashizaki, Y.				
AUTHORS	High-efficiency full-length cDNA cloning				
TITLE	Mech. Enzymol. 303, 19-44 (1999)				
JOURNAL	9279253				
MEDLINE	10349636				
PUBMED					
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
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REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Osawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PUBMED	11076861				
REFERENCE	4				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 585-590 (2001)				
REFERENCE	5				
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.				
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs				
JOURNAL	Nature 420, 563-573 (2002)				
REFERENCE	6				
AUTHORS	(bases 1 to 475)				
TITLE	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ono, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T., Segabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Direct Submission				
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN) Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,				
REFERENCE	7				
AUTHORS	AK008873				
TITLE	LOCUS				
DEFINITION	Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:221049105				
ACCESSION	AK008873				
VERSION	AK008873.1				
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	Carninci, P. and Hayashizaki, Y.				
AUTHORS	High-efficiency full-length cDNA cloning				
TITLE	Mech. Enzymol. 303, 19-44 (1999)				
JOURNAL	9279253				
MEDLINE	10349636				
PUBMED					
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
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REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Osawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
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REFERENCE	4				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 585-590 (2001)				
REFERENCE	5				
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.				
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs				
JOURNAL	Nature 420, 563-573 (2002)				
REFERENCE	6				
AUTHORS	(bases 1 to 475)				
TITLE	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y				

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES

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 Db 670 AGGATAAATTGGCTTCCCGGTTCACCGCCAGCAGTCACGGAGAGAGTTGCTGT 729
 QY 416 TTGATGACAGTGTCCGGGATTCCTCGGTGCTTCCACCCATGGCCATCGAGAACCT 475
 Db 730 TTGATGACAGTGTCCGGGATTCCTCGGTGCTTCCACCCATGGCCATCGAGAACCT 789
 QY 476 CAAGAGAGAGATGCCCTTCTAA 499
 Db 790 CAAGAGAGAGATGCCCTTCTAA 813

RESULT 15

BY076652 RIKEN full-length enriched, pooled tissues, adult spleen,
 EST. Mus musculus cDNA clone K630005115 5', mRNA sequence.
 BY076652 384 bp mRNA linear EST 06-DEC-2002

LOCUS

BY076652.1 GI:26178170

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

FEATURES

source

Location/Qualifiers

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Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shitaka, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hata, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 12466851
 22354683
 22354683
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL: http://genome.sgc.riken.go.jp/
 Aizawa, K., Akimura, T., Arakawa, I., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Nomazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

Matches	202;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 1, 2004, 13:38:44 ; Search time 20435 Seconds
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Title: US-10-030-390-2

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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ACCESSION AX069290
VERSION AX069290.1 GI:12579163
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Hans, W.C., Steidler, L. and Remaut, E.R.
TITLE Delivery of trefol peptides
JOURNAL Patent: WO 0102570-A 2 11-JAN-2001;
Vlaams Interuniversitair Instituut voor Biotechnologie (BE)

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DEFINITION Sequence 26 from patent US 6610300.
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KEYWORDS Unknown.
SOURCE ORGANISM
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 5230)
AUTHORS Segers,R.P.A.M., Waterfield,N.R., Frandsen,P.L. and Wells,J.M.
TITLE Clostridium perfringens vaccine
JOURNAL Patent: US 6610300-A 26 26-AUG-2003;
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DB	1068	TGGCTAAATAAGTAACAGGTAACGTCATTTGAATTTAGACAGTCACTTATCAACTTAT	1127	DB	2148	TAGGATGGAAACATATCAATTTCTCGAGAAATACAAATTTGAAGGATTAACATGACACTG	2207
QY	1395	CGTCAAGAAATTAAGACTGAATCTCGTGTCACTTTAATTCACCAAGATATTTCTACAGT	1454	QY	2475	GGCAAAATGAATTTAGCTCTTTTACGTATAAAGAGCCGTTTTTATCTTTAATATAACCGCT	2534
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QY	1455	TTCAATTCCTTAACAAACAGAGGTATATAATTTGGAGATATCTTACCATTTAAGCA	1514	QY	2535	CTTTTATAGAAAAATCTTAGCGTGTGTTTTTTCGAAATGCTGGCGGTACCCCAAGA	2594
DB	1188	TTCAATTCCTTAACAAACAGAGGTATATAATTTGGAGATATCTTACCATTTAAGCA	1247	DB	2268	CTTTTATAGAAAAATCTTAGCGTGTGTTTTTTCGAAATGCTGGCGGTACCCCAAGA	2327
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DB	1248	CACAAATTAATTAAGAAAGTGTGTTTTGAAAGCCATGCGTGTGACATCTATCTGATTTG	1307	DB	2328	ATTGAATAGTAGTAGATCAAAATTTATTCAGGAATAGAAATCAGAAAAATCAGATCAACCAT	2387
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QY	1995	TTATTAGGTATCTACTGACAGCTTCCAGAGGCTTAAAGAGTCCCTAGCGCTCTTATCA	2054	QY	3075	TTTCAAGTATCTAAGCTACTGAATTTAAGAAATTTGTAAGCAATCAATCGGAATCGTTTG	3134
DB	1728	TTATTAGGTATCTACTGACAGCTTCCAGAGGCTTAAAGAGTCCCTAGCGCTCTTATCA	1787	DB	2808	TTTCAAGTATCTAAGCTACTGAATTTAAGAAATTTGTAAGCAATCAATCGGAATCGTTTG	2867
QY	2055	TGGGAAGCTCGGATCATATGCAAGACAAAAATAAACTCGCAACAGCACTTGGAGAAATGG	2114	QY	3135	ATTGCTTTTTTTTGTATTTTATTAAGAGTGGAGTTTGTATGAATCATGTGAATGTAA	3194
DB	1788	TGGGAAGCTCGGATCATATGCAAGACAAAAATAAACTCGCAACAGCACTTGGAGAAATGG	1847	DB	2868	ATTGCTTTTTTTTGTATTTTATTAAGAGTGGAGTTTGTATGAATCATGTGAATGTAA	2927
QY	2115	GACGAATCGAAGAAACCTTTTACGCTGGATTTACATATCTAATAAAGCCGTTAAGGAGAC	2174	QY	3195	AACTTATATAAAAAATAGTTTTTATGGAGATAGAAAAATTTAGCAAAATCTATACACTAGA	3254
DB	1848	GACGAATCGAAGAAACCTTTTACGCTGGATTTACATATCTAATAAAGCCGTTAAGGAGAC	1907	DB	2928	AACTTATATAAAAAATAGTTTTTATGGAGATAGAAAAATTTAGCAAAATCTATACACTAGA	2987

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LOCUS Sequence 27 from patent US 6610300.
DEFINITION AR381900
ACCESSION AR381900
VERSION AR381900.1 GI:40090249
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5231)
AUTHORS Segers, R. P. A. M., Waterfield, N. R., Frandsen, P. L. and Wells, J. M.
TITLE Clostridium perfringens vaccine
JOURNAL Patent: US 6610300-A 27 26-AUG-2003;
FEATURES Location/Qualifiers
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Best Local Similarity 99.6%; Pred. No. 0;
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1521 TTATTAAGAAAGTGGTTTTGAAGCCATCGCTCTGACATCTATCTGATTTGTAAGAAAG 1580
1255 TTATTAAGAAAGTGGTTTTGAAGCCATCGCTCTGACATCTATCTGATTTGTAAGAAAG 1314
1581 GAATCTACAGCGTACTCTCGATTAATTCACCGAACACTAGGTTGCTTTGCCACACTCAAG 1640
1315 GAATCTACAGCGTACTCTCGATTAATTCACCGAACACTAGGTTGCTTTGCCACACTCAAG 1374
1641 TCTCGATTCAGCAATTCGTTTAACTGCCAGCGGAATGCTTTTCACTCTAAACCAAAAGTAA 1700
1375 TCTCGATTCAGCAATTCGTTTAACTGCCAGCGGAATGCTTTTCACTCTAAACCAAAAGTAA 1434
1701 ACAGTCTCTTAATAAAGTAACTACCGCCATACCAAGATGATCGTCAACTGTTTACTAAAG 1760
1435 ACAGTCTCTTAATAAAGTAACTACCGCCATACCAAGATGATCGTCAACTGTTTACTAAAG 1494
1761 TATATACGTAATTTGTTTCAAAATGGTCAATTCGAGAAATATCGTCAACTGTTTACTAAAG 1820
1495 TATATACGTAATTTGTTTCAAAATGGTCAATTCGAGAAATATCGTCAACTGTTTACTAAAG 1554
1821 ATCAGTTTTCATCAGCAATGAACAGCGCAAGTAAACAAATTAAGTACCGTTACTTATG 1880
1555 ATCAGTTTTCATCAGCAATGAACAGCGCAAGTAAACAAATTAAGTACCGTTACTTATG 1614
1881 AGCAAGTATTTGTTTCAAAATGGTCAATTCGAGAAATATCGTCAACTGTTTACTAAAG 1940
1615 AGCAAGTATTTGTTTCAAAATGGTCAATTCGAGAAATATCGTCAACTGTTTACTAAAG 1674
1941 AGTCCGTTTGTAAATTTGGAAGTTTACAGTTTACAGTTTAAAGGGAATGTAGATAAAATTA 2000
1675 AGTCCGTTTGTAAATTTGGAAGTTTACAGTTTACAGTTTAAAGGGAATGTAGATAAAATTA 1734
2001 GGTATACTACTGACAGCTTCCAGAGGTAAAGAGTCCCTAGCGCTCTTATCATGCGGA 2060
1735 GGTATACTACTGACAGCTTCCAGAGGTAAAGAGTCCCTAGCGCTCTTATCATGCGGA 1794
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1795 AGCTCGGATCATATGCAAGACAAAATAAATCGCAACAGCACTTCGAGAAATGGAGCGAA 1854
2121 TCGAGAAACCTCTTTAGCTGGATTACATATCTAAATAGCCGTAAAGGAGCGGGTTC 2180
1855 TCGAGAAACCTCTTTAGCTGGATTACATATCTAAATAGCCGTAAAGGAGCGGGTTC 1914
2181 AAAAGGTTTAAATAAGGAGAGCAATCAATGCAATTTAGCTAGACTATTTTTTCGAC 2240
1915 AAAAGGTTTAAATAAGGAGAGCAATCAATGCAATTTAGCTAGACTATTTTTTCGAC 1974
2241 AACGTGGAGATTTAGAGAACTGCTCTCCAGACCACTTACAAGAGCTAGTGCCTAA 2300
|||||

1975 AACGTGGAGATTTAGAGAACTGCTCTCCAAGACCAGTTTCAAAAGAGCTAGTGACATA 2034
2301 ACATATTAATTAACCGTATAAGCTGTGGAACACACTGTATATATGGAAGACCGTAGAAG 2360
2035 ACATATTAATTAACCGTATAAGCTGTGGAACACACTGTATATATGGAAGACCGTAGAAG 2094
2361 AATTAAAGCAAGAGGAGAAATTTAGAGAAATTTAATGCCATATCGTGGCGCTTAGGAT 2420
2095 AATTAAAGCAAGAGGAGAAATTTAGAGAAATTTAATGCCATATCGTGGCGCTTAGGAT 2154
2421 GGGACATATCAATTTCTTGGAGAAATCAAAATTTGAAGGATTTACATGACATCGGCGAA 2480
2155 GGGACATATCAATTTCTTGGAGAAATCAAAATTTGAAGGATTTACATGACATCGGCGAA 2214
2481 TGAATTTACGCTCTTACGTAATAAGAGCGGTTTTATTCTTAATTAACCGCTCTTTTT 2540
2215 TGAATTTACGCTCTTACGTAATAAGAGCGGTTTTATTCTTAATTAACCGCTCTTTTT 2274
2541 ATAGAAAAAATTCCTTTAGCGTGGTTTTTTTCGAAATGCTGGCGGTACCCCAAGAAATAGA 2600
2275 ATAGAAAAAATTCCTTTAGCGTGGTTTTTTTCGAAATGCTGGCGGTACCCCAAGAAATAGA 2334
2601 AATGAGTAGATCAAAATTTACGAATAGAAATCAGGAAAAATCAGATCCAAACATAAARAC 2660
2335 AATGAGTAGATCAAAATTTACGAATAGAAATCAGGAAAAATCAGATCCAAACATAAARAC 2394
2661 ACTAGAACAAAATTCGAAAGTTAACTAATCAACCTAGTAGTGGATTTAATCCCAATAGA 2720
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2721 GCCAACAGAACAGAGCGCAGAAACAGAAATCAGAACTAGAAATCAGATTTAGAAATGGA 2780
2455 GCCAACAGAACAGAGCGCAGAAACAGAAATCAGAACTAGAAATCAGATTTAGAAATGGA 2514
2781 AGAAGAAAAAGCAATGACTTCTGTTGAATTAATCAGCAAAATCGTGTCTATTTTTTTTT 2840
2515 AGAAGAAAAAGCAATGACTTCTGTTGAATTAATCAGCAAAATCGTGTCTATTTTTTTTT 2574
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2575 AAAAGCGGTATACCTAGATATAACGAAACAGAACTGAATAGAAACGAAAGAGCGAT 2634
2901 GACACATTTATAAATGTTTGAACACATTTTATAAATGCATAGCCCATAGATTTGCCAA 2960
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2961 ACCAACCGTTATCAGTTAGTCAGATGAATCTTCCCTCGTAAAGATTTAATTAACCT 3020
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2755 TTGTTTGAAGACCGGTATATAACCGTACTATCATTTATAGGAAATCAATCGGAAATCGTTGATGCT 2814
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2815 GTATCTAAGCTACTGAATTTAAGAAATTTAAGCAATCAATCGGAAATCGTTGATGCT 2874
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2875 TTTTGTATTTTATAGAGGTGGAGTTTGTATGAATCATGATGAATGTAAAACTTA 2934
3201 TATAAAAAATPAGTTTATTTGGAGATAAGAAAAATAGCAAAATCTATACACTAGAAACGTT 3260
2935 TATAAAAAATPAGTTTATTTGGAGATAAGAAAAATAGCAAAATCTATACACTAGAAACGTT 2994
3261 TAGAAAGAGTTAGAAAAAGAAATCTACTTTAGAAAAAATAAATAATGATTAATTTTC 3320
2995 TAGAAAGAGTTAGAAAAAGAAATCTACTTTAGAAAAAATAAATAATGATTAATTTTC 3054
3321 TTCCGAGGGGAGATTTATATATAGTTTAATAGAAAAATAAATAATGATTAATTTTC 3380
3055 TTCCGAGGGGAGATTTATATATAGTTTAATAGAAAAATAAATAATGATTAATTTTC 3114

QY 3381 TAGTGGAAGAAATGACTTATAAGAGGAAAAATCTTTTCAAAACATGCAATATTGAA 3440
Db 3115 TAGTGGAAGAAATGACTTATAAGAGGAAAAATCTTTTCAAAACATGCAATATTGAA 3174
QY 3441 ACAGTTGATGAAAGCAACCAAGTAAATTAACACCTATTATTATAGATTATAGG 3500
Db 3175 ACAGTTGATGAAAGCAACCAAGTAAATTAACACCTATTATTATAGATTATAGG 3234
QY 3501 AAAGGAGAACAGCTGAATGAATATCCCTTTTGTGTGAGAACTGTCTTCATGACGCTT 3560
Db 3235 AAAGGAGAACAGCTGAATGAATATCCCTTTTGTGTGAGAACTGTCTTCATGACGCTT 3294
QY 3561 GTTAAAGTACAAATTTAAATATAGTAAATTCGCTCAATCACTACCAAGCCAGGTAAAG 3620
Db 3295 GTTAAAGTACAAATTTAAATATAGTAAATTCGCTCAATCACTACCAAGCCAGGTAAAG 3354
QY 3621 CAAAGGGGCTATTTTGGCTATCGCTCAAAATCAAGCATGATGCGCGTGTGTGTGT 3680
Db 3355 CAAAGGGGCTATTTTGGCTATCGCTCAAAATCAAGCATGATGCGCGTGTGTGTGT 3414
QY 3681 TCTGACTCCGAGGAGCGATTCAAGAAATCAAGATACATTTACATTCGACACCCAA 3740
Db 3415 TCTGACTCCGAGGAGCGATTCAAGAAATCAAGATACATTTACATTCGACACCCAA 3474
QY 3741 CGTTTATCGTTATGGAACGTATGACAGAGGAAAAACCGTTTATACACGAAAGCAATTCGA 3800
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QY 3801 AAACAATTTAAGCAATCAATACCTCTTTTATGATTTTATGATTTACAGCGCAAGA 3860
Db 3535 AAACAATTTAAGCAATCAATACCTCTTTTATGATTTTATGATTTACAGCGCAAGA 3594
QY 3861 AACTATTTTCAAGCAAGCATATTTTAAACACCGCTATTTAGTTAGTTTATGCTACTAT 3920
Db 3595 AACTATTTTCAAGCAAGCATATTTTAAACACCGCTATTTAGTTAGTTTATGCTACTAT 3654
QY 3921 GATTATCAATCTGATTAAGGTATCAAGCATATTTTGTGTTTATGAGACCGCATATGT 3980
Db 3655 GATTATCAATCTGATTAAGGTATCAAGCATATTTTGTGTTTATGAGACCGCATATGT 3714
QY 3981 GACTTCAAAATCAGAAATTTAAATCTGTCAAGAGCCCAAAATATTTTCGCAAAATATCCG 4040
Db 3715 GACTTCAAAATCAGAAATTTAAATCTGTCAAGAGCCCAAAATATTTTCGCAAAATATCCG 3774
QY 4041 AGAATATTTTGAAGTCTTTGCCAGTTGATCTAACGTGTAATCATTTTGGTATGCTCG 4100
Db 3775 AGAATATTTTGAAGTCTTTGCCAGTTGATCTAACGTGTAATCATTTTGGTATGCTCG 3834
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Db 3835 CATACCAAGACCGGCAATGTAGAAATTTTGTATCCTAATTTACCGTTATTTCTTTCAAAGA 3894
QY 4161 ATGGCAAGTTCGCTCTTCAACCAACAGATAATTAAGGGCTTTACTCGTTCAGTCTAAC 4220
Db 3895 ATGGCAAGTTCGCTCTTCAACCAACAGATAATTAAGGGCTTTACTCGTTCAGTCTAAC 3954
QY 4221 GGTTTTAAAGCGGTACAGAGGCAAAACCAAGTAGATGAACCCCTGGTTTAACTCTTTAT 4280
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QY 4401 TCAGTTTATATATCATGATACACCTTACAGAGAAAGAGATATCAAAATCTGTAG 4460
Db 4135 TCAGTTTATATATCATGATACACCTTACAGAGAAAGAGATATCAAAATCTGTAG 4194

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Db 4195 AAGTGCCTATTTCAGAAACATATCAAGGGCTAATAGGAAATACATTACCATCTCTTTGCAA 4254
QY 4521 AGCTTGGGTATCAAGTGAATTAACCACTAAAGATTTATTTGTCCTCAAGGGTGGTTTAA 4580
Db 4255 AGCTTGGGTATCAAGTGAATTAACCACTAAAGATTTATTTGTCCTCAAGGGTGGTTTAA 4314
QY 4581 ATTCAAGAAAAAAGAGCGAAAGCTCAACGCTGTCTAATTTGTCAGAAATGAAGAAAGATTT 4640
Db 4315 ATTCAAGAAAAAAGAGCGAAAGCTCAACGCTGTCTAATTTGTCAGAAATGAAGAAAGATTT 4374
QY 4641 AATGCTTTATATTAGCGAAAAAGCGATGATACAGCCCTTATTTAGTGACGACCAAAAA 4700
Db 4375 AATGCTTTATATTAGCGAAAAAGCGATGATACAGCCCTTATTTAGTGACGACCAAAAA 4434
QY 4701 AGAGATTAGAGAAAGTGTAGCGATTCTCTGAAACGCAATTAGATAAATTTGCTGAAGTACT 4760
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QY 4761 GAAGCGAATCAGGAAATTTTCTTTAAGATTAAACAGGAGAAATGCTGGCAATCAACT 4820
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QY 4821 TGCTAGTGTAAATCAATTTGCTATCGATCAATTAAGTAAAAAAGAGAAAAAGAAAG 4880
Db 4555 TGCTAGTGTAAATCAATTTGCTATCGATCAATTAAGTAAAAAAGAGAAAAAGAAAG 4614
QY 4881 CTATATAAGCGCTGACAAATTTCTTTTGAATTTAGAGCATACATTCTATTCAAGAGACTTT 4940
Db 4615 CTATATAAGCGCTGACAAATTTCTTTTGAATTTAGAGCATACATTCTATTCAAGAGACTTT 4674
QY 4941 AAAAAGCTAGCAGACGCGCTAAAAACGCAACAACAATCTGATTTGTTTGTATGATAC 5000
Db 4675 AAAAAGCTAGCAGACGCGCTAAAAACGCAACAACAATCTGATTTGTTTGTATGATAC 4734
QY 5001 AGGCTGAAAAATAAACCCGCACTATGCCATTACATTATATCTATGATACGTTGTTT 5060
Db 4735 AGGCTGAAAAATAAACCCGCACTATGCCATTACATTATATCTATGATACGTTGTTT 4794
QY 5061 TTTCTTTGCTTTTGTAGCGAATGATTTAGCAGAAATATACAGATTAAGTTTAAATTA 5120
Db 4795 TTTCTTTGCTTTTGTAGCGAATGATTTAGCAGAAATATACAGATTAAGTTTAAATTA 4854
QY 5121 TTAGGGGAGAGAGAGAGTAGCCCGAAAACTTTTGTGCTTGGCTTGGACTGAAACGAAGTG 5180
Db 4855 TTAGGGGAGAGAGAGAGTAGCCCGAAAACTTTTGTGCTTGGCTTGGACTGAAACGAAGTG 4914
QY 5181 AGGAAAGGCTACTAAAAACGTCGAGGGGAGTGAGAGCGAGCAACCTGATTTTAA 5240
Db 4915 AGGAAAGGCTACTAAAAACGTCGAGGGGAGTGAGAGCGAGCAACCTGATTTTAA 4974
QY 5241 ATTTTCTATCTTTTATAGGTCATTAGAGTACTTATTTGCTCTATAAACTATTTAGCAG 5300
Db 4975 ATTTTCTATCTTTTATAGGTCATTAGAGTACTTATTTGCTCTATAAACTATTTAGCAG 5034
QY 5301 CATATAGATTATTTGAATAGGTCATTAAAGTTGACATATTAGAGGAGAAAACTCTGG 5360
Db 5035 CATATAGATTATTTGAATAGGTCATTAAAGTTGACATATTAGAGGAGAAAACTCTGG 5094
QY 5361 AGAATATTTGAAGAACCCGATTTACATGATGATTTGCTTGTGTTAGTCTGTTT 5420
Db 5095 AGAATATTTGAAGAACCCGATTTACATGATGATTTGCTTGTGTTAGTCTGTTT 5154
QY 5421 TAACATAAGTAGGAAATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5480
Db 5155 TAACATAAGTAGGAAATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5214
QY 5481 GTCAAGGTGATTAATA 5497
Db 5215 GTCAAGGTGATTAATA 5231

[illegible]

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QY 2361 AATTAAAGCAAGAGAGAGATTTAGAGAGATTTAATGCCATATGCGTGGCGGTAGGAT 2420
Db 2095 AATTAAAGCAAGAGAGAGATTTAGAGAGATTTAATGCCATATGCGTGGCGGTAGGAT 2154
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Db 2155 GGAACATATCAATTTCTTGAGATACAAATTTGAAGGATATACATGACACTGGGAAA 2214
QY 2481 TGAATTTAGCTCTTTACGTATATAAAGAGCCGTTTTATTCTTAATATAACCGCTCTTTTT 2540
Db 2215 TGAATTTAGCTCTTTACGTATATAAAGAGCCGTTTTATTCTTAATATAACCGCTCTTTTT 2274
QY 2541 ATAGAAAAATCTTAGCGTGGTTTTTTCGAAATGCTGGCGGTACCCCAAGATTAGA 2600
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Db 2335 AATGAGTAGATCAAAATTTATTCAGATAGAAATCAGAAAAATCAGATCCAAACATATAAAAC 2394
QY 2661 ACTAGAACAAATGCAAGTTAACTTAACCTAACGCTAGTAGGATTTAATCCCAATGA 2720
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Db 2455 GCCAACAGAACAGAGCCAGAACAGAAATCAGAACAGTAACATTTGGATTTAGAAATGGA 2514
QY 2781 AGAGAAAAAGCAATGCTTGTGTGAATTAATGACCAAGATCGTGGCTATTTTTTTT 2840
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QY 2841 AAAAGCGGTATCTAGATATACGAAACAAAGCACTGAATAGAACGAAAGAGCCAT 2900
Db 2575 AAAAGCGGTATCTAGATATACGAAACAAAGCACTGAATAGAACGAGCCAT 2634
QY 2901 GACATTTTATAAATGTTGACGACATTTTATAATGCATAGCCGATAGATTTGCCAA 2960
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QY 2961 ACCAAGCGTTATCAGTTAGTACAGATGAATCTTCCCTCGTAAGAGATTTAATTAAC 3020
Db 2695 ACCAAGCGTTATCAGTTAGTACAGATGAATCTTCCCTCGTAAGAGATTTAATTAAC 2754
QY 3021 TTGTTTGAAGCGGTATATACCGTACTATCATNTATATAGGAAATCAGAGAGTTTCAA 3080
Db 2755 TTGTTTGAAGCGGTATATACCGTACTATCATNTATATAGGAAATCAGAGAGTTTCAA 2814
QY 3081 GTATCTAAGCTACTGAAATTTAGAAATTTGTAAGCAATCAATCGGAAATCGTTGATGCT 3140
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Db 2875 TTTTGTGTTATCATTTATAGAGGTGGATTTGTATGATCATGATCAATGTAAGACTTA 2934
QY 3201 TATAAAAAATAGTTTTTGGAGATAGAAAAATAGCAAAATATCTATACCTAGAAAGCTT 3260
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Db 2995 TAAGAAAGGTAGAAAAAGAGAAATATCTCTAGAAACAAATCAGATAGATTTTTTC 3054
QY 3321 TTCGGAGGGGAGATTTATATATAAGTTAATAGAAATAACAAAAATATTTTTCGAT 3380
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QY 3381 TAGTGGAAAAAATTCGACTTATAAGGAAAAAATCTTTTTCAAAAATGCAATATTGAA 3440

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Db 3355 CAAGGGGCTATTTTTCGGTATCGCTCAAAATCAAGCATGATTTGGCGGTGCTGCTGCTTGT 3414
QY 3681 TCTGACTTTCCGAGGAAGCGATTTCAAGAAAAATCAAGATACATTTTACACATTGGAACCCAA 3740
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QY 3741 CGTTTATCGTTATGGAACGATGTCAGACGAAACCGTTTCATACAGAAAGGACATTTCTGA 3800
Db 3475 CGTTTATCGTTATGGAACGATGTCAGACGAAACCGTTTCATACAGAAAGGACATTTCTGA 3534
QY 3801 AAACAATTTAAGACAAATCAATACCTTTTATTGATTTTGTGATTTTACACAGCCAAAGA 3860
Db 3535 AAACAATTTAAGACAAATCAATACCTTTTATTGATTTTGTGATTTTACACAGCCAAAGA 3594
QY 3861 AACTATTTTCAGACGAGCATTTTAAACACCGTATTTGATTTAGGTTTATGCTACTAT 3920
Db 3595 AACTATTTTCAGACGAGCATTTTAAACACCGTATTTGATTTAGGTTTATGCTACTAT 3654
QY 3921 GATTATCAAAATCTGATAAGGTTTATCAAGCATATTTTGTGTTTGAACCCAGCTPATCT 3980
Db 3655 GATTATCAAAATCTGATAAGGTTTATCAAGCATATTTTGTGTTTGAACCCAGCTPATCT 3714
QY 3981 GACTTCAAAATCAAGATTTAAATCTGTCRAAGCAGCCAAATTAATTTCCGAAATATCCG 4040
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QY 4041 AGAATATTTTGGAAAGCTTTTGGCAGTTGATCTAACGTTAATCATTTTGGTATGCTCG 4100
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Db 3835 CATACCGAGAACGACATGATAGAAATTTTGTGATCTTAATTCCTGTTATTTCTTCAAAGA 3894
QY 4161 ATGCAAGATTTGGTCTTTTCAAAACAAAGATTAATAGGGCTTTTACTCGTTCAAGTCTAAC 4220
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QY 4401 TGAGTTTAAATACGATTAAGTCAACCCCTTGAAGAAAAAGAGTAAATCAAAATTTGTTAG 4460
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QY 4461 AAGTGCCTTATTCAGAAACCTATCAAGGGGCTAATAGGGAATACATTTACCATTCTTTGCAA 4520

4195	Db	AGTGCCTATTTCAGAAAACTATCAAGGGGCTAATAGGGAATACATTACCANTCTTTGCGAA	4255
4521	Qy	AGCTTGGGTATCAAGTGATTTAAACCAGTAAGAATTTATTTGTCGGTCAAGGGTGGTTTAA	4580
4255	Db	AGCTTGGGTATCAAGTGATTTAAACCAGTAAGAATTTATTTGTCGGTCAAGGGTGGTTTAA	4314
4581	Qy	ATTCAAGAAAAAAGAGCGAACGTCGAAAGCTGTCATTTGTCAGATGGAAGAGATTT	4640
4315	Db	ATTCAAGAAAAAAGAGCGAACGTCGAAAGCTGTCATTTGTCAGATGGAAGAGATTT	4374
4641	Qy	AATGGCTTATATTAGCGAAAAAAGCGATGATACAAGCCCTTATTAGTGACGACCAAAAA	4700
4375	Db	AATGGCTTATATTAGCGAAAAAAGCGATGATACAAGCCCTTATTAGTGACGACCAAAAA	4434
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4435	Db	AGAGATTAGAGAGTCTTAGGCCATTCCTGAACGGACATTAGATAAATTCGCTGAAGTACT	4494
4761	Qy	GAAGGCCAATCAGGAAATTTCTTTAAGATTAACAGGAAGAAATGCTGGCATTTCAACT	4820
4495	Db	GAAGGCCAATCAGGAAATTTCTTTAAGATTAACAGGAAGAAATGCTGGCATTTCAACT	4554
4821	Qy	TGCTAGTGTTAAATCATGTTGCTATCGATCATTAAGATTAAAAAAGAGAAAGAAAG	4880
4555	Db	TGCTAGTGTTAAATCATGTTGCTATCGATCATTAAGATTAAAAAAGAGAAAGAAAG	4614
4881	Qy	CTATATAAAGCGCCTGACAAATTTCTTTGACTTTAGAGCATACATTCATTCAAGAGACTTT	4940
4615	Db	CTATATAAAGCGCCTGACAAATTTCTTTGACTTTAGAGCATACATTCATTCAAGAGACTTT	4674
4941	Qy	ARACAAGCTAGCAGAACGCCCTAAACGGACACACAACCTCGATTTGTTAGCTATCATAC	5000
4675	Db	ARACAAGCTAGCAGAACGCCCTAAACGGACACACAACCTCGATTTGTTAGCTATCATAC	4734
5001	Qy	AGGCTGAAATAAAACCCCGCACTATGCCATTACATTTATATCTATGATACGTTGTTT	5060
4735	Db	AGGCTGAAATAAAACCCCGCACTATGCCATTACATTTATATCTATGATACGTTGTTT	4794
5061	Qy	TTTCTTTGCTGTTTACGGAATGATTAGCAAAATATACAGAGTAAGATTTTAATTAATTA	5120
4795	Db	TTTCTTTGCTGTTTACGGAATGATTAGCAAAATATACAGAGTAAGATTTTAATTAATTA	4854
5121	Qy	TTAGGGGAGAAAGAGAGTAGTCCCGAAACCTTTTAGTTGGCTTGGACTGAACGAAGTG	5180
4855	Db	TTAGGGGAGAAAGAGAGTAGTCCCGAAACCTTTTAGTTGGCTTGGACTGAACGAAGTG	4914
5181	Qy	AGGGAAGGCTACTAAACCTGCAGGGGCGAGTCAGACGGAAGCGACACTTGTATTTTTTA	5240
4915	Db	AGGGAAGGCTACTAAACCTGCAGGGGCGAGTCAGACGGAAGCGACACTTGTATTTTTTA	4974
5241	Qy	ATTTTCTATCTTTTATAGGTCATTAGAGTATACCTTATTTGTCCTATAAACTATTTAGCAG	5300
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5361	Qy	AGAAATATTGGAAGAACCCGATTACATGGATTCGATTTCTTTGTTGGTTACGTGGTTT	5420
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5421	Qy	TAACATAAAGCTAGTGAATTTTTCGATTTTTCGCTGCTGCTGCTGTTGTTAGTATTTGCTA	5480
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5481	Qy	GTCAAAGTGATTTAAATA	5497
5215	Db	GTCAAAGTGATTTAAATA	5231

RESULT 8
AF038666

181	Db		AAGACTATGGATCAATAGTTTGTAGAAAAAGATGTGATCCGTAGCGGTTTTCAAAATTTGCA	240
898	Qy		ACCAGGAATGAATTAACHTATCCCTTTTATCAAGAAAGCGCAAAAGAAAAACGAATATGATACA	957
241	Db		ACCAGGAATGAATTAACHTATCCCTTTTATCAAGAAAGCGCAAAAGAAAAACGAATATGATACA	300
958	Qy		CCAAATCAGTGCMAAAAAAGATATTAATGGGAGATAAGACGGTTCTGTCTCGTCTGACTTG	1017
301	Db		CCAATCAGTGCMAAAAAAGATATTAATGGGAGATAAGACGGTTCTGTCTCGTCTGACTTG	360
1018	Qy		CACCATATCATAAAAATTCGAAACAGCAAAAGATGGCGGAAACGTAAAGAAAGTTATGGAA	1077
361	Db		CACCATATCATAAAAATTCGAAACAGCAAAAGATGGCGGAAACGTAAAGAAAGTTATGGAA	420
1078	Qy		ATAAGACTTTAGAAGCAAACTTTAAGAGTGTGTGTAGTAGTGCAGTATCTTAAAAATTTTGTAT	1137
421	Db		ATAAGACTTTAGAAGCAAACTTTAAGAGTGTGTGTAGTAGTGCAGTATCTTAAAAATTTTGTAT	480
1138	Qy		AATAGGAATTCGAAGTTAAATTTAGATGCTAAAAATTTGTAAATTAAGAAGAGTAGTATACAT	1197
481	Db		AATAGGAATTCGAAGTTAAATTTAGATGCTAAAAATTTGTAAATTAAGAAGAGTAGTATACAT	540
1198	Qy		GAAACAAAAATAAAAATATTCTCAAAACTTTTTTAAACGAGTGA AAAAGTACTCAACCAAAAT	1257
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661	Db		GCAATTAACGACGAAATCGGCTAAAAATAAGTAACAGGTAAACGTCTATTGCAATTTAGACAG	720
1378	Qy		TCATCTATTCAACTTATCGTCAGAAAAATTA AAAACGTAATCTCGTGCTCACTTTAAATTC	1437
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901	Db		CATCTATCTGATTTGGAAGAGATTTCTACAGCGGTACCTTGATATTCACCGAACACT	960
1618	Qy		AGGGTGTCTTTGCACACTCAAGTCTCGATTTCAGCAATTTGCTTAAGCTGCCAGCGGAATG	1677
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1918	Qy		TAAACGGAGGAAATAAATCTATAGTCCGCTTTTGTAAATTTGGAAAGTTACACGTTACTA	1977

1261	Db	TAACGGGAGGAAATAATCTATGAGTCGCTTTTGTGTAATTTGGAAAGTTACACGTTACTA	1321
1978	Qy	AAGGGAATGTAGATAAAATATTATTAGGTATACCTGACAGCTTCCCAAGGAGCTAAAGAGGT	2037
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1391	Db	AGCACTTGGAGAAATGGACGAATCGAGAAAAACCTCTTTTACGCTGGATTACATATCTAA	1422
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1956	Db	AATAGAAAACAAAAGACGCATGACACATTTTATAAATGTTTTGACGACATTTTATAAAT	2015
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2016	Db	GCATAGCCCGATTAAGATTGCAAAACCAACCGCTTTATCAGTTTAGTCAGATGAACCTCTCCCT	2075
2998	Qy	CGTAAGAAGTTATTTAAATTAACCTTTGTTTGAAGACGGTATATAAACGCTACTCATTTATA	3057
2076	Db	CGTAAGAAGTTATTTAAATTAACCTTTGTTTGAAGACGGTATATAAACGCTACTCATTTATA	2135


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Db      4356 AAGTGATTAATA 4368

RESULT 10
AF007787
LOCUS   AF007787      8199 bp    DNA        linear    BCT 19-JUN-1998
DEFINITION Enterococcus faecalis plasmid pAM-beta-1 copy number repressor
            (copf), repE (rep), resolvase (res beta), and type I
            topoisomerase (top beta) genes, complete cds and unknown genes.
ACCESSION AF007787 X17092
VERSION   AF007787.1 GI:3023041
KEYWORDS
SOURCE   Enterococcus faecalis
ORGANISM Enterococcus faecalis
          Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
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REFERENCE 1 (bases 1 to 5100)
AUTHORS Swinfield,T.J., Oultram,J.D., Thompson,D.E., Br hm,J.K. and
          Minton,N.P.
TITLE     Physical characterisation of the replication region of the
          Streptococcus faecalis plasmid pAM beta 1
JOURNAL  Gene 87 (1), 79-90 (1990)
MEDLINE  90236302
PUBMED   2110101
REFERENCE 2 (bases 5095 to 7223)
AUTHORS Swinfield,T.J., Janniere,L., Ehrlich,S.D. and Minton,N.P.
TITLE     Characterization of a region of the Enterococcus faecalis plasmid
          pAM beta 1 which enhances the segregational stability of pAM beta
          1-derived cloning vectors in Bacillus subtilis
JOURNAL  Plasmid 26 (3), 209-221 (1991)
MEDLINE  92094042
PUBMED   1661428
REFERENCE 3 (bases 1 to 8199)
AUTHORS Bidnenko,V., Ehrlich,S.D. and Janniere,L.
TITLE     In vivo relations between pAMBeta1-encoded type I topoisomerase and
          plasmid replication
JOURNAL  Mol. Microbiol. 28 (5), 1005-1016 (1998)
MEDLINE  98326819
PUBMED   9663686
REFERENCE 4 (bases 1 to 8199)
AUTHORS Bidnenko,V.
TITLE     Direct Submission
COMMENT   Submitted (10-JUN-1997) Genetique Microbienne, INRA, Domaine de
FEATURES Vilvert, Jouy en Josas 78352, France
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3925 ACCTCATGTTTACCTCTCTTTAGCCTTCTTTAGTTTCAAGGCTATTCATCAACCAAGCTGGG 3984
4388 AATATAATATGTTGAGTTTAAATATCGATTAAGTATCAACCTTTAGAGAAAGAAAGTAA 4447
3985 AATATAATATGTTGAGTTTAAATATCGATTAAGTATCAACCTTTAGAGAAAGAAAGTAA 4044
4448 TCAGAAATGTTAGAGGCTTATTCAGAAACCTATCAAGGCGCTATAGGGAATACATTA 4507
4045 TCAGAAATGTTAGAGGCTTATTCAGAAACCTATCAAGGCGCTATAGGGAATACATTA 4104
4508 CCATCTCTTCAAGCTTGGGTATCAAGTATTAACCAAGTAAAGGTTATTTGTCGGTC 4567
4105 CCATCTCTTCAAGCTTGGGTATCAAGTATTAACCAAGTAAAGGTTATTTGTCGGTC 4164
4568 AAGGCTGTTTAAATTCAGAAAGAAAGCAAGCTCAAGCTGTTTCAATTTGTCGAAT 4627
4165 AAGGCTGTTTAAATTCAGAAAGAAAGCAAGCTCAAGCTGTTTCAATTTGTCGAAT 4224
4628 GGAAAGAGATTTAATGCTTATATAGCGAAAGGCGATGATACAGCCCTTATTTAG 4687
4225 GGAAAGAGATTTAATGCTTATATAGCGAAAGGCGATGATACAGCCCTTATTTAG 4284
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4748 TGCTGAAGGTACTGAAGCGCAATCAGGAAATTTTCTTTAGATTAACCAAGGAGAAATG 4807
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QY 4988 TTAGCTATGATACAGGCTGAAAAATAAAACCGGCACTATGCCATTACATTTATCTATGA 5047
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QY 5108 TTTTAAATTAATTTATGAGGCGAGAGAGAGTAGCCCGGAAACCTTTTAGTTGCTTTGG 5167
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Db 5005 GTTACGCTGTTTAACTAAAGTAGTGAATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTG 5064
QY 5468 TTAGTATTTGCTAGTCAAGGATTAATA 5497
Db 5065 TTAGTATTTGCTAGTCAAGGATTAATA 5094

RESULT 11

AF041239

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

AF041239 4963 bp DNA circular SYN 16-JAN-1998
Cloning vector pIL253 replication protein D (repD), replication
protein E (repE), and adenine methylase (ermAM) genes, complete cds
and complete sequence.
AF041239
AF041239.1 GI:2773391
Cloning vector pIL253
Cloning vector pIL253
artificial sequences; vectors.
1 (bases 1 to 4963)
Simon,D. and Chopin,A.
Construction of a vector plasmid family and its use for molecular
cloning in Streptococcus lactis
Biochimie 70 (4); 559-566 (1988)
89000956
PUBMED 2844302
2 (bases 1 to 4963)
Chopin,A.
Direct Submission
Submitted (06-JAN-1998) Genetique Microbienne, INRA, Domaine de
Villvert, Jouy-en-Josas 78352, France
Location/Qualifiers
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/organism="Cloning vector pIL253"
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/db_xref="taxon:71279"
/note="high copy number cloning vector for Gram-positive
bacteria; derived from cloning vector pIL252, GenBank

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	494..793	/note="repD"
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	/protein_id="AAB96787.1"	
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	/translation="WNHDECKTYIKNSLLLEIRKLIANYLTLETFFKLEKRNIVLETKS	
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	836..2326	/note="repE"
	/gene="repE"	
	/codon_start=1	
	/transl_table=11	
	/product="replication protein E"	
	/protein_id="AAB96788.1"	
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	/translation="WNIPFVVEVTVLHDLGLKYPKNSKIRSIITTKPKSKGAIPAVRS	
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	TKKEIRVLGIPERTLQKLVKANOIEFKIKPGRNGGIQIASVKSLLLSIIKVKK	
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	CFHPKPVNSVLIILKTRHTDVPDKYWKLYTFYFVKWVNRREYRQLFTFNGPHOMKHA	
	KVNLSLTVTYEQVLISFNYSLLFNGRK"	
ORIGIN		
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Best Local Similarity		100.0%; Pred No. 0;
Matches 2816; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
QY	2682	AACAACTCAACGCTAGTAGTGATTTAATCCCAATAGAGCCAAACAGAGCCGAGA 2741
DB	1	AACAACTCAACGCTAGTAGTGATTTAATCCCAATAGAGCCAAACAGAGCCGAGA 60
QY	2742	RACGAATCAGAACCAAGTAACATGGATTAGAAATGGAAGCAAGAAAGCAATGACTT 2801
DB	61	AACGAATCAGAACCAAGTAACATGGATTAGAAATGGAAGCAAGAAAGCAATGACTT 120
QY	2802	CGTGTGAATAATGACGAATCGTTGCTTTATTTTTTAAAGCGGTATCTAGATATA 2861
DB	121	CGTGTGAATAATGACGAATCGTTGCTTTATTTTTTAAAGCGGTATCTAGATATA 180
QY	2862	ACGAACACGAACTGAATAGAACGAAAGAGCCCATGACATTTATAAATGTTTG 2921
DB	181	ACGAACACGAACTGAATAGAACGAAAGAGCCCATGACATTTATAAATGTTTG 240
QY	2922	ACGACATTTTATAATGATAGCCGATAAGATTGCCAAACCAACCGCTTATCAGTTAGTC 2981
DB	241	ACGACATTTTATAATGATAGCCGATAAGATTGCCAAACCAACCGCTTATCAGTTAGTC 300

QY	2982	AGATGAACCTCTTCCCTCGTAAGAAGTATTATTAATTAACCTTTGTTGAAGCGGTATATAA 3041
DB	301	AGATGAACCTCTTCCCTCGTAAGAAGTATTATTAATTAACCTTTGTTGAAGCGGTATATAA 360
QY	3042	CCGTACTATCATTATATATAGGGAATCAGAGAGTTTCAAGTATCTTAAGCTACTGAATTA 3101
DB	361	CCGTACTATCATTATATATAGGGAATCAGAGAGTTTCAAGTATCTTAAGCTACTGAATTA 420
QY	3102	AGAAATGTTTAAAGCAATCAATCGGAATCGTTTGAATGCTTTTGTATTCAATTTATAGA 3161
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QY	3162	AGGTGGAGTTTGTATGAATCATATGAATGTAAACCTTATATAAATAATAGTTTATGGA 3221
DB	481	AGGTGGAGTTTGTATGAATCATATGAATGTAAACCTTATATAAATAATAGTTTATGGA 540
QY	3222	GATAAGAAAATTTAGCAAAATATCTATACACTAGAAAAGTAAAGAAAGAGTTAGAAAAGAG 3281
DB	541	GATAAGAAAATTTAGCAAAATATCTATACACTAGAAAAGTAAAGAAAGAGTTAGAAAAGAG 600
QY	3282	AAATATCTACTTAGAAAAAAAATCAGATAAGTATTTTCTTCGGAGGGGGGAAGATTATAT 3341
DB	601	AAATATCTACTTAGAAAAAAAATCAGATAAGTATTTTCTTCGGAGGGGGGAAGATTATAT 660
QY	3342	ATATAAGTTTAAAGAAAATAACAAATAATTTTATTCGATTAGTGGAATAAATTTGACTTA 3401
DB	661	ATATAAGTTTAAAGAAAATAACAAATAATTTTATTCGATTAGTGGAATAAATTTGACTTA 720
QY	3402	TAAAGAAAAAAATCTTTTCAAAACATGCAATATTTGAAACAGTTTGAATGAAAAGCAAA 3461
DB	721	TAAAGAAAAAAATCTTTTCAAAACATGCAATATTTGAAACAGTTTGAATGAAAAGCAAA 780
QY	3462	CCAAGTTTAAATTAACCAACTATTTTATAGGATTTATAGGAAGAGACACGCTGAATGAA 3521
DB	781	CCAAGTTTAAATTAACCAACTATTTTATAGGATTTATAGGAAGAGACACGCTGAATGAA 840
QY	3522	TATCCCTTTTGTGTAGAAAACCTGCTTTCATGACGGCTTGTAAAGTACAAATTTAAAAA 3581
DB	841	TATCCCTTTTGTGTAGAAAACCTGCTTTCATGACGGCTTGTAAAGTACAAATTTAAAAA 900
QY	3582	TAGTAAATTCGCTCAATCATACCAAGCCAGGTAAGAACGAGGGCTATTTTGGCTA 3641
DB	901	TAGTAAATTCGCTCAATCATACCAAGCCAGGTAAGAACGAGGGCTATTTTGGCTA 960
QY	3642	TCGCTCAAAATCAAGCATGATTGGCGGTCTGCTGCTTCTGACTTCGAGGAGCGAT 3701
DB	961	TCGCTCAAAATCAAGCATGATTGGCGGTCTGCTGCTTCTGACTTCGAGGAGCGAT 1020
QY	3702	TCAAGAAAATCAAGTATACATTTCATGAGCACCCCAACGTTTATCGTTATGGNACGTA 3761
DB	1021	TCAAGAAAATCAAGTATACATTTCATGAGCACCCCAACGTTTATCGTTATGGNACGTA 1080
QY	3762	TGCAGACGAAACCGTTCATACACGAAAGGACATTTCTGAAAACATTTTAAAGCAATCAA 3821
DB	1081	TGCAGACGAAACCGTTCATACACGAAAGGACATTTCTGAAAACATTTTAAAGCAATCAA 1140
QY	3822	TACCTTCTTTTATGATTTTATATTTTCAACGCAAAAGAAACTATTTTCAAGAACGATAT 3881
DB	1141	TACCTTCTTTTATGATTTTATATTTTCAACGCAAAAGAAACTATTTTCAAGAACGATAT 1200
QY	3882	TTTAAACACCGTATTTGATTAGGTTTATGCTACTATGATTATCAATCTGATAAAGG 3941
DB	1201	TTTAAACACCGTATTTGATTAGGTTTATGCTACTATGATTATCAATCTGATAAAGG 1260
QY	3942	TTATCAAGCATATTTTGTATTTAGAAAACCGCAGTCTATGTGACTTCAAAATCAGAAATTA 4001
DB	1261	TTATCAAGCATATTTTGTATTTAGAAAACCGCAGTCTATGTGACTTCAAAATCAGAAATTA 1320
QY	4002	ATCTGTCAAGACGACCAAAATATTTTCGAAAATATCCGAAATATTTTGGAAAGTCTTT 4061
DB	1321	ATCTGTCAAGACGACCAAAATATTTTCGAAAATATTTTCGAAATATTTTGGAAAGTCTTT 1380

QY 4062 GCCAGTTCATTAACGCTGTAATCAATTTTGGTATTCGTCGCATACCAAGAACGGAACAATGT 4121
DB 1381 GCCAGTTCATTAACGCTGTAATCAATTTTGGTATTCGTCGCATACCAAGAACGGAACAATGT 1440
QY 4122 AGAATTTTTCATCTTAATACCGTTATCTTTTCAAGAGATGCGAAGATTGCTTTCAA 4181
DB 1441 AGAATTTTTCATCTTAATACCGTTATCTTTCAAGAGATGCGAAGATTGCTTTCAA 1500
QY 4182 ACAAACAGATTAATAGGCTTTTACTCGTTCAGTCTAAGCTTAACCGTTTAAAGCGGTACAGAAGG 4241
DB 1501 ACAAACAGATTAATAGGCTTTTACTCGTTCAGTCTAAGCTTAACCGTTTAAAGCGGTACAGAAGG 1560
QY 4242 CAAAAACAAGTACGATGACCCCTGGTTTAACTCTTATTCGACGAAACGAAATTTTCAGG 4301
DB 1561 CAAAAACAAGTACGATGACCCCTGGTTTAACTCTTATTCGACGAAACGAAATTTTCAGG 1620
QY 4302 AGAAAGGGTTTAAATAGGCGGTAATAACGTCATGTTTACCCCTCTCTTTAGCCTACITTAG 4361
DB 1621 AGAAAGGGTTTAAATAGGCGGTAATAACGTCATGTTTACCCCTCTCTTTAGCCTACITTAG 1680
QY 4362 TTCAGGCTATTCATCGAAAGCTGCGAATATAATATGTTTGAAGTTTAAATATCGATTAGA 4421
DB 1681 TTCAGGCTATTCATCGAAAGCTGCGAATATAATATGTTTGAAGTTTAAATATCGATTAGA 1740
QY 4422 TCACCCCTTAGAAGAAAGAAAGTAATCAAAATTTTGAAGTGCCTATTTCAGAAACTA 4481
DB 1741 TCACCCCTTAGAAGAAAGAAAGTAATCAAAATTTTGAAGTGCCTATTTCAGAAACTA 1800
QY 4482 TCAGGGGCTTAATAGGGAATACATACATCTTTGCAAGCTTGGGTATCAAGTCAATTT 4541
DB 1801 TCAGGGGCTTAATAGGGAATACATACATCTTTGCAAGCTTGGGTATCAAGTCAATTT 1860
QY 4542 AACCACTAAAGATTATTTTGCCTCAAGGTGTTTAAATTCAGAAAGAAAGGACCGA 4601
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QY 4602 ACCTCAACGCTTCATTTGTCAGAAAGAAAGATTTTAAATGCTTATATTCAGCAAAA 4661
DB 1921 ACCTCAACGCTTCATTTGTCAGAAAGAAAGATTTTAAATGCTTATATTCAGCAAAA 1980
QY 4662 AAGCGATGATACAGGCTTTATTTAGTACGACCAAAAGAGATTTAGAGAGTGTAGG 4721
DB 1981 AAGCGATGATACAGGCTTTATTTAGTACGACCAAAAGAGATTTAGAGAGTGTAGG 2040
QY 4722 CATTCCTGAACGGACATTAGATAAATGCTGAAGTACTGAAGCGCAATCAGGAAATTTT 4781
DB 2041 CATTCCTGAACGGACATTAGATAAATGCTGAAGTACTGAAGCGCAATCAGGAAATTTT 2100
QY 4782 CTTTAAAGATTAAACCGAGAGAAATGCTGGCATTCACCTTGTAGTGTAAATCATTTGT 4841
DB 2101 CTTTAAAGATTAAACCGAGAGAAATGCTGGCATTCACCTTGTAGTGTAAATCATTTGT 2160
QY 4842 GCTATCGATCATTAAGTAAAAAGAAAGAAAGAAAGCTATATAAGCGCTGACAAA 4901
DB 2161 GCTATCGATCATTAAGTAAAAAGAAAGAAAGAAAGCTATATAAGCGCTGACAAA 2220
QY 4902 TCTTTTGCATTAGAGATACATTCATTCAGAGACTTTTAAACAAGCTAGCAGAACGCC 4961
DB 2221 TCTTTTGCATTAGAGATACATTCATTCAGAGACTTTTAAACAAGCTAGCAGAACGCC 2280
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QY 5022 CTATGCCATTACATTTATCTATGATACGCTGTTGTTTCTTTGCTGTTTAGCGAAT 5081
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QY 5082 GATTAGCAGAAATATACAGAGTAAGATTTTAAATTAATATAGGGGAGAGAGAGAGT 5141
DB 2401 GATTAGCAGAAATATACAGAGTAAGATTTTAAATTAATATAGGGGAGAGAGAGAGT 2460
QY 5142 AGCCCGAAAACTTTTAGTTGGCTTGACTCAACGAAGTACGAGGAAAGGCTACTAAAACGT 5201

DB 2461 AGCCCGAAAACTTTTAGTTGGCTTGACTGAACGAAGTACGAGGAAAGGCTACTAAAACGT 2520
QY 5202 CGAGGGGAGTGCAGAGCGAAGCAACATTTGATTTTAAATTTCTATCTTTTATAGGTC 5261
DB 2521 CGAGGGGAGTGCAGAGCGAAGCAACATTTGATTTTAAATTTCTATCTTTTATAGGTC 2580
QY 5262 ATTAGAGTATACATTTTCTCTATAAATCTATTAGCAGCATATAGATTTTATGAATAG 5321
DB 2581 ATTAGAGTATACATTTTCTCTATAAATCTATTAGCAGCATATAGATTTTATGAATAG 2640
QY 5322 GTCATTTAAGTTGAGCATATTAGAGAGGAAATCTTGGAGAAATATTGGAAGACCCGA 5381
DB 2641 GTCATTTAAGTTGAGCATATTAGAGAGGAAATCTTGGAGAAATATTGGAAGACCCGA 2700
QY 5382 TTACATGGAATTCGATTTAGTTCTTGTGTTTACGTGTTTAACTAAAGTACTGAATTTT 5441
DB 2701 TTACATGGAATTCGATTTAGTTCTTGTGTTTACGTGTTTAACTAAAGTACTGAATTTT 2760
QY 5442 TGATTTTGGTGTGTGTCTTGTGTTTGTAGTATTTGCTAGTCAAAAGTGAATAATA 5497
DB 2761 TGATTTTGGTGTGTGTCTTGTGTTTGTAGTATTTGCTAGTCAAAAGTGAATAATA 2816

RESULT 12

AF039139

LOCUS

DEFINITION

AF039139

Cloning vector pIL252

protein E (repE), and adenine methylase (ermA) genes, complete cds.

AF039139

VERSION

AF039139.1

Cloning vector pIL252

artificial sequences; vectors.

REFERENCE

1 (bases 1 to 4698)

AUTHORS

Simon, D. and Chopin, A.

TITLE

Construction of a vector plasmid family and its use for molecular

cloning in *Streptococcus lactis*

JOURNAL

MEDLINE

PUBMED

REFERENCE

2 (bases 1 to 4698)

AUTHORS

Chopin, A.

TITLE

Direct Submission

JOURNAL

Vilvert, J.

Submitted (18-DEC-1997)

Genetique Microbienne, INRA, Domaine de

Location/Qualifiers

1. 4698

/organism="Cloning vector pIL252"

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/lab_host="Enterococcus faecalis"

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494. .793

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1741 TCAACCCCTTAGAGAAAAGAGTAATCAAAATGTTAGAGTGCCTATTAGAAAACCTA 1800
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4602 ACGTCAACGCTGTTCAATTTGTCAGAAATGGAAGAGATTTAATGCTTTATATTAGCGAAA 4661
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2161 GCTATCGATCATTAAGTAAGAAAAGAGAAAGAAAGAGCTATATAAGCGCGTGCACAA 2220
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2221 TTCTTTGACTAGAGATACATTCATTCAAGAGACTTTAAACAAGCTAGCAGAACGCC 2280
4962 TAAACGGAACACACTCGATTTGTTAGCTAGTATACAGGCTGAAATATAAACCCGCA 5021
2281 TAAACGGAACACACTCGATTTGTTAGCTAGTATACAGGCTGAAATATAAACCCGCA 2340
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2341 CTATGCCATTACATTTATATCTATGATACGCTGTTTCTTTCTTCTGCTTTAGCGAAT 2400
5082 GATTAGCAGAAATATACAGAGTAAGATTTTAAATTAATTATAGGGGAGAGAGAGAGT 5141
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5142 AGCCCGAAACTTTTAGTTGGCTTGGACTGAACGAGTGGGAAAGGCTACTAAAACGT 5201
2461 AGCCCGAAACTTTTAGTTGGCTTGGACTGAACGAGTGGGAAAGGCTACTAAAACGT 2520
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2521 CGAGGGCAGTGAAGCGAAGCAACACTTTGATTTTAAATTTCTATCTTTTATAGGTC 2580
5262 ATTAGATATACATTTTGTCTTATATACTATTAGCAGCATTAATAGATTTATGATAG 5321
2581 ATTAGATATACATTTTGTCTTATATACTATTAGCAGCATTAATAGATTTATGATAG 2640
5322 GTCAATTTAAGTTGAGCATATTAGAGAGGAAATCTTTGGAGAAATATTGAAGAACCGCA 5381
2641 GTCAATTTAAGTTGAGCATATTAGAGAGGAAATCTTTGGAGAAATATTGAAGAACCGCA 2700
5382 TTACATGATGATTAAGTTCTTTGCTGTTACGTTGTTTAACTAAAGAGTAGTGAATTTT 5441
2701 TTACATGATGATTAAGTTCTTTGCTGTTACGTTGTTTAACTAAAGAGTAGTGAATTTT 2760
5442 TGATTTTGGTGTGTGCTTCTGTTAGTATTTCCTAGTCAAGTGAATTAATA 5497

Db 2761 TGATTTTGGTGTGTGCTTCTGTTAGTATTTCCTAGTCAAGTGAATTAATA 2816

RESULT 13
AY303237/c
LOCUS
DEFINITION
Shuttle vector pLEIIdt+KR''deltaORF, complete sequence.
ACCESSION
AY303237
VERSION
AY303237.1 GI:32185266
KEYWORDS
Shuttle vector pLEIIdt+KR''deltaORF
SOURCE
Shuttle vector pLEIIdt+KR''deltaORF
ORGANISM
artificial sequences; vectors.
REFERENCE
1 (bases 1 to 11925)
Staddon,J.H.
TITLE
L1.ltrB group II intron donor plasmid with a large deletion in the
intron encoded protein ORF, ltrA
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 11925)
Staddon,J.H.
AUTHORS
Direct Submission
TITLE
Submitted (19-MAY-2003) Microbiology, University of Minnesota, MMC
JOURNAL
196, 420 Delaware Street S.E., Minneapolis, MN 55455, USA
FEATURES
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1..11925
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/mol_type="genomic DNA"
/db_xref="taxon:234876"
1623..1802
/note="ltrBE1; partial exon"
/number=1
1803..4225
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tddelta(1-3)"
2376..2585
/note="maturase with internal deletion"
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RESULT 14
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LOCUS
DEFINITION Shuttle vector pLEIttd+KR'', complete sequence.
ACCESSION AY303236
VERSION AY303236.1 GI:32140767
KEYWORDS
SOURCE Shuttle vector pLEIttd+KR''
ORGANISM Shuttle vector pLEIttd+KR''
REFERENCE artificial sequences; vectors.
AUTHORS 1 (bases 1 to 13515)
TITLE Cousineau,B., Lawrence,S., Smith,D. and Belfort,M.
JOURNAL Retrotransposition of a bacterial group II intron
MEDLINE Nature 404 (6781), 1018-1021 (2000)
PUBMED 20259072
REFERENCE 2 (bases 1 to 13515)
AUTHORS Staddon,O.H.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2003) Microbiology, University of Minnesota, MMC
FEATURES 196, 420 Delaware Street S.E., Minneapolis, MN 55455, USA
SOURCE Location/Qualifiers.
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RESULT 15

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LOCUS X64695
DEFINITION X64695.1 GI:456362
ACCESSION erm1 gene; erm2 gene; ORF; reps gene.
VERSION Streptococcus pyogenes
KEYWORDS
SOURCE

9084 bp DNA linear BCT 10-FEB-1999

SPPLASS

S.pyogenes plasmid pBT233 sequence (reps to ermI).

LOCUS

X64695

DEFINITION

X64695.1

GI:456362

erm1 gene; erm2 gene; ORF; reps gene.

VERSION

Streptococcus pyogenes

KEYWORDS

SOURCE

ORGANISM Streptococcus pyogenes
 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 Streptococcus.
 REFERENCE 1 (bases 1 to 9084)
 AUTHORS Ceglowski, P., Boitsov, A., Chai, S., and Alonso, J.C.
 TITLE Analysis of the stabilization system of pSM19035-derived plasmid
 pB233 in *Bacillus subtilis*
 JOURNAL Gene 136 (1-2), 1-12 (1993)
 MEDLINE 94123985
 PUBMED 8293991
 REFERENCE 2 (bases 1 to 9084)
 AUTHORS Alonso, J.C.
 TITLE Direct Submission
 JOURNAL Submitted (27-FEB-1992) J.C. Alonso, Max-Planck-Institut fuer
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QY	5168	ACTGAAACGAGTGAAGGAAAGGCTACTAAACGTCGAGGGGCGAGTAGAGCGAAGC	5227
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QY	5228	ACTGATTTTAAATTTCTATCTTTTATAGTCAATTAGATATACTTATTGTCCTATA	5287
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QY	5288	AACCTATTTAGCAGCATATAATAGATTTATTGAATAGGTCATTTAAAGTTGAGCATATTAGAGG	5347
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DB	2333	GATCAAGAATGAAAAATTTTATTTA	2357

Search completed: September 1, 2004, 20:41:02
Job time : 20461 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 1, 2004, 13:08:39 ; Search time 1889 Seconds
(without alignments)
12362.279 Million cell updates/sec

Title: US-10-030-390-2
Perfect score: 5497
Sequence: 1 gaattgattagtcatttt.....ctagtcgaagtattataaata 5497

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 segs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseq1990s:.*
3: Geneseq2000s:.*
4: Geneseq2001as:.*
5: Geneseq2001bs:.*
6: Geneseq2002as:.*
7: Geneseq2003as:.*
8: Geneseq2003bs:.*
9: Geneseq2003cs:.*
10: Geneseq2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	5497	100.0	5497	5	AAF29646		Aat29646 Plasmid p
2	5010.8	91.2	5770	3	AAA15043		Aa15043 Nucleotid
3	5001.4	91.0	5906	3	AAA15042		Aa15042 Nucleotid
4	4999	90.9	5870	3	AAA15044		Aa15044 Nucleotid
5	4993.4	90.8	5230	3	AAx07549		Aax07549 pTREX1 mu
6	4991.8	90.8	5230	3	AAA15041		Aa15041 Nucleotid
7	4982.4	90.6	5216	2	AAx07548		Aax07548 pK390 TIR
8	4944.6	90.0	5231	2	AAx07550		Aax07550 pTREX1A m
9	1434.8	26.1	3765	2	AAx13224		Aax13224 Enterococ
10	1434.8	26.1	3765	6	ABS99019		Ab99019 Enterococ
11	1111	20.2	10323	2	AAx90954		Aax90954 Plant tra
12	1111	20.2	17111	3	AAx01289		Aax01289 Arabidops
13	1111	20.2	17116	3	AAx01290		Aax01290 Arabidops
14	1109.4	20.2	10929	6	ABK98591		ABK98591 pE25 vec
15	1109.4	20.2	10929	8	ACD13842		ACD13842 Plasmid p
16	983.6	17.9	15676	3	AAx01288		Aax01288 Arabidops
17	884	16.1	6243	2	AAZ09598		Aaz09598 Clostridi
18	876.6	15.9	9412	6	ABK98635		ABK98635 Vector pE
19	876.6	15.9	9412	6	ABK98636		ABK98636 Vector pE
20	876.6	15.9	9412	8	ACD13886		ACD13886 L. lactis
21	876.6	15.9	9412	8	ACD13887		ACD13887 L. lactis
22	876.6	15.9	9417	6	ABK98632		ABK98632 Vector pE
23	876.6	15.9	9417	8	ACD13883		ACD13883 L. lactis

C 24	876.6	15.9	9425	6	ABK98630		ABK98630 Vector pE
C 25	876.6	15.9	9425	8	ACD13881		ACD13881 L. lactis
C 26	876.6	15.9	9437	6	ABK98601		ABK98601 Vector pE
C 27	876.6	15.9	9437	8	ACD13852		ACD13852 Xyl opera
C 28	876.6	15.9	9484	6	ABK98633		ABK98633 Vector pE
C 29	876.6	15.9	9484	8	ACD13884		ACD13884 L. lactis
C 30	876.6	15.9	9566	6	ABK98634		ABK98634 Vector pE
C 31	876.6	15.9	9566	8	ACD13885		ACD13885 L. lactis
C 32	876.6	15.9	12733	6	ABK98631		ABK98631 Vector pE
C 33	876.6	15.9	12733	8	ACD13882		ACD13882 L. lactis
C 34	876.6	15.9	12739	6	ABK98592		ABK98592 Vector pE
C 35	876.6	15.9	12739	8	ACD13843		ACD13843 Plasmid p
C 36	833.8	15.2	9749	2	AAx13091		Aax13091 Enterococ
C 37	833.8	15.2	9749	6	ABS98886		AB98886 Enterococ
C 38	747	13.6	747	6	ABK78393		ABK78393 Bacillus
C 39	731.6	13.3	738	2	AAV37113		Aav37113 Antibioti
C 40	731.6	13.3	738	4	AAH01718		Aah01718 Escherich
C 41	471	8.6	5142	5	AAF29645		Aaf29645 Plasmid p
C 42	381	6.9	381	6	ABK73933		ABK73933 Bacillus
C 43	295.6	5.4	4995	7	AAx51077		Aax51077 pOTHY16 p
C 44	295.6	5.4	6964	7	AAx51073		Aax51073 Lactococc
C 45	293	5.3	6904	7	AAx51072		Aax51072 Lactococc

ALIGNMENTS

RESULT 1
AAF29646
ID AAF29646 standard; DNA; 5497 BP.

XX AC AAF29646;
XX XX
DT 10-APR-2001 (first entry)
XX DE Plasmid pTMTFF1.

XX Mouse TFF1; mTFF; trefoil protein; antiinflammatory; gastrointestinal;
XX anti-ulcer; peptide therapy; gastrointestinal disease; acute colitis;
KW Crohn's disease; ulcerative colitis; plasmid pTMTFF1;
KW recombinant vector; ds.
XX OS Synthetic.

XX WC200102570-A1.
XX 11-JAN-2001.
XX 05-JUL-2000; 2000WO-EP006343.
XX 05-JUL-1999; 99EP-00870143.

XX (VLA--) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX Hans WC, Steidler L, Remaut ER;
XX WPI; 2001-138142/14.
XX Recombinant Lactococcus lactis for delivering a trefoil peptide useful
PT for treating acute or chronic gastrointestinal inflammatory diseases or
PT disorders, e.g. acute or ulcerative colitis, acute flare-ups of Crohn's
PT disease.

XX Claim 18; Fig 1c; 44pp; English.

XX The present sequence is a recombinant vector which may be used to
CC generate a recombinant Lactococcus lactis capable of delivering a trefoil
CC peptide in vivo. The recombinant microorganism is useful for
CC manufacturing an agent for the delivery of a trefoil peptide to the
CC gastrointestinal tract, and for treating gastric or intestinal diseases
CC or disorders, or lesions caused by gastric or intestinal diseases or
CC disorders. The microorganism may also be used for preparing medicament to
CC be used for treating gastric and /or gastrointestinal diseases or

CC disorders, acute gastrointestinal inflammatory diseases (e.g., acute
 CC colitis, acute flare-ups of Crohn's diseases, or ulcerative colitis), and
 CC chronic and spontaneously recurring diseases of the gastrointestinal
 CC tract comprising Crohn's disease (enteritis regionalis) and ulcerative
 CC colitis (colitis ulcerosa). Disease states which can be treated by the
 CC method or compositions comprising the recombinant microorganism or
 CC trefoil peptides include disorders of and damage to the alimentary canal,
 CC including the mouth, esophagus, stomach and large and small intestine,
 CC as well as for the protection and treatment of tissues that lie outside
 CC the alimentary canal
 XX
 SQ Sequence 5497 BP; 1994 A; 870 C; 1051 G; 1582 T; 0 U; 0 Other;

Query Match 100.0%; Score 5497; DB 5; Length 5497;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	61	TTTTTATAATTAATCTATAAACCATATCCCTCTTTGGAAATCAAAATTTATATCTACTCC	120
QY	121	TTTGTAGATATCTTATAATACAGTATCAGATCTGGGAGACCAACCGTTTCCACTAG	180
DB	121	TTTGTAGATATCTTATAATACAGTATCAGATCTGGGAGACCAACCGTTTCCACTAG	180
QY	181	AAATAATTTGTTTAACTTTAGAAAGGAGATATACGATGAAAAAAGATTATCTCAGC	240
DB	181	AAATAATTTGTTTAACTTTAGAAAGGAGATATACGATGAAAAAAGATTATCTCAGC	240
QY	241	TATTTTAAATGCTACAGTCATATTTCTGCTGCGACCCCGTTGTCAGTGTTTACGCCCA	300
DB	241	TATTTTAAATGCTACAGTCATATTTCTGCTGCGACCCCGTTGTCAGTGTTTACGCCCA	300
QY	301	GGCCAGGCCAGGCCAGGCCAGGAAACAATGATATATGCCCCCGGGAGAGGAT	360
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DB	361	AAATTTGCTGCTCCCGGTGTACCGCCAGAGTGCAGGAGAGGTTGCTGTTTGA	420
QY	421	TGACAGTGTCCGGGATTTCCCGTGTGTCTCCACCCATGCCATCGAGAACACTCAAGA	480
DB	421	TGACAGTGTCCGGGATTTCCCGTGTGTCTCCACCCATGCCATCGAGAACACTCAAGA	480
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DB	481	AGAAGAAATGCTCTTAATAGTAGATCCGGCTGCTAAACAGCCCGAAGAGAGCTGA	540
QY	541	GTGTGCTGCTGCCAGCTGAGCAATTAATAGCATAACCCCTTGGGCGCTCTTAAACGGGT	600
DB	541	GTGTGCTGCTGCCAGCTGAGCAATTAATAGCATAACCCCTTGGGCGCTCTTAAACGGGT	600
QY	601	CTTGAGGGGTTTTTGTCTGAAGAGGAACTATATCCGGATGACCTCGAGCAAGCTCTA	660
DB	601	CTTGAGGGGTTTTTGTCTGAAGAGGAACTATATCCGGATGACCTCGAGCAAGCTCTA	660
QY	661	GAATCGATACGATTTTGAAGTGGCAACAGATATAAAGAGAGTTTAAATTTGTTCTGA	720
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QY	721	ACTTTTAAAAAACAAGCAATAAATCATTTGTCGAACAGATAGCGACAGAGAGCGGAAAA	780
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QY	781	CATTGCTGCTGCTCATTTCAATAGCAATGCTTTTCTTAAAGATATAAAGCTATTAAG	840
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QY	841	ACTATGATCAATAGTTTGAAGAAAGATGTATCCCTAGCGGTTTTTCAAAATTTGCAACC	900
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QY	901	AGGAATGAATTAATCTATCCCTTTTATCAAGAGCGGCAAGAAAGAAAGCAATGATACCA	960
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QY	1141	AGGAATTTGAAGTTAAATTAAGATGCTTAAATTTTGAATTTGAAGAGGATGATACGAA	1200
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QY	1261	AAAAAATTTAAATTTAAAGAAACCGATACCTTTTACGAAATTTGAAACAGGTAAAGGCA	1320
DB	1261	AAAAAATTTAAATTTAAAGAAACCGATACCTTTTACGAAATTTGAAACAGGTAAAGGCA	1320
QY	1321	TTTAAACGAGCAAACTGGCTTAAATTAAGTAAACAGGTAAAGTCTTAAATTTAGACAGTCA	1380
DB	1321	TTTAAACGAGCAAACTGGCTTAAATTAAGTAAACAGGTAAAGTCTTAAATTTAGACAGTCA	1380
QY	1381	TCTATTCAACTTATCGTCAGAAAAATTTAAACACTGAAATCTCGTGTCACTTTAAATTCACCA	1440
DB	1381	TCTATTCAACTTATCGTCAGAAAAATTTAAACACTGAAATCTCGTGTCACTTTAAATTCACCA	1440
QY	1441	AGATATTTACAGTTTCAATTTCCCTTAAACAGAGGTATATAAATTTGGAGAGTATCC	1500
DB	1441	AGATATTTACAGTTTCAATTTCCCTTAAACAGAGGTATATAAATTTGGAGAGTATCC	1500
QY	1501	TTACCAATTTAAGCACACAAATTTATTAAGTGTGTTTTTGAAGCCATGGCTCTGACAT	1560
DB	1501	TTACCAATTTAAGCACACAAATTTATTAAGTGTGTTTTTGAAGCCATGGCTCTGACAT	1560
QY	1561	CTATCTGATTTTGAAGAGGATTTCTACAGGTACCTTGGATTTTACCCGCACTAGG	1620
DB	1561	CTATCTGATTTTGAAGAGGATTTCTACAGGTACCTTGGATTTTACCCGCACTAGG	1620
QY	1621	GTGTGCTTGCACACTCAAGTCTCGAATTCAGCAATTTGCTTAAGCTGCGAGCGGATGCTT	1680
DB	1621	GTGTGCTTGCACACTCAAGTCTCGAATTCAGCAATTTGCTTAAGCTGCGAGCGGATGCTT	1680
QY	1681	TCATCTTAAACCAAAAGTAAACAGTGTCTTAAATAAACTTTACCCGCCATACACAGATGT	1740
DB	1681	TCATCTTAAACCAAAAGTAAACAGTGTCTTAAATAAACTTTACCCGCCATACACAGATGT	1740
QY	1741	TCAGATAAATTTGGAAGCTATATACGTAATTTGCTTAAATAAGTGGTCAATCGAGATA	1800
DB	1741	TCAGATAAATTTGGAAGCTATATACGTAATTTGCTTAAATAAGTGGTCAATCGAGATA	1800
QY	1801	TCGTCAACTGTTTACTTAAATTCAGTTTTCATCAAGCAATGAAACACGCCAAGTAAACAA	1860
DB	1801	TCGTCAACTGTTTACTTAAATTCAGTTTTCATCAAGCAATGAAACACGCCAAGTAAACAA	1860
QY	1861	TTTAAAGTACCGTTACTTATGAGCAAGTATCTCTATTTTAAATTTTAAATTTTAA	1920
DB	1861	TTTAAAGTACCGTTACTTATGAGCAAGTATCTCTATTTTAAATTTTAAATTTTAA	1920
QY	1921	CGGAGGAAATAATTTCTATGATGCTGCTTTTGTAAATTTTGAAGAGTTACAGCTTAAAG	1980

1921	Db	CGGGAGGAATTAATCTTATGAGTCGCTTTTGTGTAATTTGGAAAGTTACACGTTACTTAAAG	1980
1981	Qy	GGAACTGAGATAAATTTAGGTATACTGTGACAGCTTCCAAGGAGCTTAAAGAGGTCCC	2040
1981	Db	GGAACTGAGATAAATTTAGGTATACTGTGACAGCTTCCAAGGAGCTTAAGAGGTCCC	2040
2041	Qy	TAGCGTCTTTATCATGGGAAAGCTCGATCATATGCAAGACAAAAATAAATCGCAACAGC	2100
2041	Db	TAGCGTCTTTATCATGGGAAAGCTCGATCATATGCAAGACAAAAATAAATCGCAACAGC	2100
2101	Qy	ACTTTGAGAAATGGGACGAAATCAGAAAAACCCCTTTTACGTGGATTACATATCTAATAA	2160
2101	Db	ACTTTGAGAAATGGGACGAAATCAGAAAAACCCCTTTTACGTGGATTACATATCTAATAA	2160
2161	Qy	AGCGCTAAGGAGACGGGTTCAAAAAGGTTTAAATAAAGGAGAGCAATCAATGCATTAGC	2220
2161	Db	AGCGCTAAGGAGACGGGTTCAAAAAGGTTTAAATAAAGGAGAGCAATCAATGCATTAGC	2220
2221	Qy	TAGAACTATATTTTGGACAACTGGAGAAATTTAGAGAACGTCCTCCAAGACAGATT	2280
2221	Db	TAGAACTATATTTTGGACAACTGGAGAAATTTAGAGAACGTCCTCCAAGACAGATT	2280
2281	Qy	ACAAAGAGCTAGTGCCTAAACATAATTTAAACGCTATAAGTGTGTGGAACTGTATA	2340
2281	Db	ACAAAGAGCTAGTGCCTAAACATAATTTAAACGCTATAAGTGTGTGGAACTGTATA	2340
2341	Qy	TATGAAAAAGCCGTAGAGAAATTTAAAGCAAGAGAGAAATTTAGAGAGATTTAATGCC	2400
2341	Db	TATGAAAAAGCCGTAGAGAAATTTAAAGCAAGAGAGAAATTTAGAGAGATTTAATGCC	2400
2401	Qy	ATATGGTGGCCGTAGGATGGAAACATATCAATTTTCTTGGAGATACAAATTTTCAAGG	2460
2401	Db	ATATGGTGGCCGTAGGATGGAAACATATCAATTTTCTTGGAGATACAAATTTTCAAGG	2460
2461	Qy	ATPACATGACACTGGGCAATGAATTTACGTCCTTTACGTPATAAAAAGACGGTTTATTC	2520
2461	Db	ATPACATGACACTGGGCAATGAATTTACGTCCTTTACGTPATAAAAAGACGGTTTATTC	2520
2521	Qy	TTAATATAAGCGCTCTTTTATAGAAAAAATCCTTAGCGTGGTTTTTTTCCGAAATGCTG	2580
2521	Db	TTAATATAAGCGCTCTTTTATAGAAAAAATCCTTAGCGTGGTTTTTTTCCGAAATGCTG	2580
2581	Qy	GCGGTACCCCAAGAAATTAGAAATGAGTAGATCAAAATTTATTCAGAAATAGAAATCAGAAAA	2640
2581	Db	GCGGTACCCCAAGAAATTAGAAATGAGTAGATCAAAATTTATTCAGAAATAGAAATCAGAAAA	2640
2641	Qy	TCAGATCCACCATATAAACACTAGAACAAATTTGCAAGTTAACTAACTCAACGCTAGTA	2700
2641	Db	TCAGATCCACCATATAAACACTAGAACAAATTTGCAAGTTAACTAACTCAACGCTAGTA	2700
2701	Qy	GTGGATTTAATCCCAATGAGCCAAACAGAACCCAGAGCCAGAAAAACAGAAATCAGAAACAGTA	2760
2701	Db	GTGGATTTAATCCCAATGAGCCAAACAGAACCCAGAGCCAGAAAAACAGAAATCAGAAACAGTA	2760
2761	Qy	ACATTTGATTTAGAAATGGAAGAGAAAAAGCAATGACTTCGTGTGAATAATATGACGAA	2820
2761	Db	ACATTTGATTTAGAAATGGAAGAGAAAAAGCAATGACTTCGTGTGAATAATATGACGAA	2820
2821	Qy	ATCGTTCCTTATTTTTTTTAAAAGCGGTATACCTAGATATAACGAAACCAACGAACTGAAT	2880
2821	Db	ATCGTTCCTTATTTTTTTTAAAAGCGGTATACCTAGATATAACGAAACCAACGAACTGAAT	2880
2881	Qy	AGAAACGAAAAAGAGCCATGACACATTTATAAAATGTTTGCACGACATTTTATAAATGCA	2940
2881	Db	AGAAACGAAAAAGAGCCATGACACATTTATAAAATGTTTGCACGACATTTTATAAATGCA	2940
2941	Qy	TAGCCCGATGAAGTTGCAACCAACGCTTATCAGTTAGTCAGATGAACCTCTTCCCTCGT	3000
2941	Db	TAGCCCGATGAAGTTGCAACCAACGCTTATCAGTTAGTCAGATGAACCTCTTCCCTCGT	3000
3001	Qy	AAGAAGTTATTTAATTAACCTTGTGTTGAAGACGGTATATACCGCTACTATCATATATAG	3060

Db	3001	AAGAAGTTATTTAACTTTGTTTGAAGACGGTATATAAACCGTACTATCATTTATATAG	3061
Qy	3061	GGAAATCAGAGAGTCTTCAAGTATCTAAGCTACTGAAATTTAAGAAATGTTTAAGCAATCAA	3120
Db	3061	GGAAATCAGAGAGTCTTCAAGTATCTAAGCTACTGAAATTTAAGAAATGTTTAAGCAATCAA	3120
Qy	3121	TCGGAAATCGTTTGATGCTTTTTTGTATTCATTTATAGNAGGTGGAGTTTGTATGAAT	3180
Db	3121	TCGGAAATCGTTTGATGCTTTTTTGTATTCATTTATAGNAGGTGGAGTTTGTATGAAT	3180
Qy	3181	CATGATGAATGTAAAACTTTATATAAAAAATAGTTTATTCGAGATAAGAAAAATPAGCAAAAT	3240
Db	3181	CATGATGAATGTAAAACTTTATATAAAAAATAGTTTATTCGAGATAAGAAAAATPAGCAAAAT	3240
Qy	3241	ATCTATACACTAGAAACGTTTAAAGAGAGTTAGAAAAAGAGAAATATCTACTTTAGAAAAACA	3300
Db	3241	ATCTATACACTAGAAACGTTTAAAGAGAGTTAGAAAAAGAGAAATATCTACTTTAGAAAAACA	3300
Qy	3301	AAATCAGATAAGTATTTTTCTTCGGAGGGGGAAGATTATATATAAGTTAAATAGAAAAAT	3360
Db	3301	AAATCAGATAAGTATTTTTCTTCGGAGGGGGAAGATTATATATAAGTTAAATAGAAAAAT	3360
Qy	3361	AACAAAATAATTTATTCGATTAGTGCAAAAAAAATTCACCTTATAAGGAAAAAAAATCTTTT	3420
Db	3361	AACAAAATAATTTATTCGATTAGTGCAAAAAAAATTCACCTTATAAGGAAAAAAAATCTTTT	3420
Qy	3421	TCAAAAATCGCATATTTGAAACAGTTGAAATGAAAAAGCAAAACCAAGTTAATTTAAACAAC	3480
Db	3421	TCAAAAATCGCATATTTGAAACAGTTGAAATGAAAAAGCAAAACCAAGTTAATTTAAACAAC	3480
Qy	3481	TATTTTATAGGATTTATAGGAAAGGAGAACAGCTGAATGAATATCCCTTTGTGTAGAA	3540
Db	3481	TATTTTATAGGATTTATAGGAAAGGAGAACAGCTGAATGAATATCCCTTTGTGTAGAA	3540
Qy	3541	ACTGTGCTTCATGACGGCTTGTTTAAAGTAGTACAATTTTAAAAATAGTAAAAATTCGCTCAATC	3600
Db	3541	ACTGTGCTTCATGACGGCTTGTTTAAAGTAGTACAATTTTAAAAATAGTAAAAATTCGCTCAATC	3600
Qy	3601	ACTACCAAGCCAGTAAAAAGCAAAAGGGGTATTTTTCGGTATCGCTCAAAATCAAGCATG	3660
Db	3601	ACTACCAAGCCAGTAAAGCAAAAGGGGTATTTTTCGGTATCGCTCAAAATCAAGCATG	3660
Qy	3661	ATTGGCGGTGCTGGTGTGTTCTGACTTTCGAGGAAGCGATTCAGAAAAATCAAGATACA	3720
Db	3661	ATTGGCGGTGCTGGTGTGTTCTGACTTTCGAGGAAGCGATTCAGAAAAATCAAGATACA	3720
Qy	3721	TTTACACATTTGGACACCCAAACGTTTATCGTTATGGAACGTTATGCACACGAAAAACCGTTCA	3780
Db	3721	TTTACACATTTGGACACCCAAACGTTTATCGTTATGGAACGTTATGCACACGAAAAACCGTTCA	3780
Qy	3781	TACACGAAAGGACATTTCTGAAAACAATTTAAGACAAATCAATACCTTCTTTATGATTTT	3840
Db	3781	TACACGAAAGGACATTTCTGAAAACAATTTAAGACAAATCAATACCTTCTTTATGATTTT	3840
Qy	3841	GATATTCACACGGCAAAAGAAACTATTTTCAGCAAGCGATATTTTAAACAACCGCTATTGAT	3900
Db	3841	GATATTCACACGGCAAAAGAAACTATTTTCAGCAAGCGATATTTTAAACAACCGCTATTGAT	3900
Qy	3901	TTAGGTTTTATGCGCTACTATGATTTATCAAAATCTGATAAAGGTTATCAAGCATATTTTGT	3960
Db	3901	TTAGGTTTTATGCGCTACTATGATTTATCAAAATCTGATAAAGGTTATCAAGCATATTTTGT	3960
Qy	3961	TTAGAAACGCCAGTCTATGTGACTTCAAATCAGANTTTAAATCTGTCAGAACGAGCCAAA	4020
Db	3961	TTAGAAACGCCAGTCTATGTGACTTCAAATCAGANTTTAAATCTGTCAGAACGAGCCAAA	4020
Qy	4021	ATAATTTGCAAAATATCCGAGAAATTTTGGAAAAGTCTTTTGGCAGTTGATCTAAACGTGT	4080
Db	4021	ATAATTTGCAAAATATCCGAGAAATTTTGGAAAAGTCTTTTGGCAGTTGATCTAAACGTGT	4080
Qy	4081	AATCATTTTGGTATTCGTCGCATACCAAGAACGACATGTAGAAATTTTGTGATCTCTAAT	4140
Db	4081	AATCATTTTGGTATTCGTCGCATACCAAGAACGACATGTAGAAATTTTGTGATCTCTAAT	4140

Query Match		91.2%	Score 5010.8	DB 3	Length 5770		
Best Local Similarity		100.0%	Pred. No. 0				
Matches 5002		Conservative 0	Mismatches 0	Indels 0	Gaps 0		
Qy	496	CTAAGTATAGTATCCGGTCTGTATCAAGAGCCGAAAGAGAGCTGAGTGGTCTGCGCAC	555				
Db	769	CTAAGTATAGTATCCGGTCTGTATCAAGAGCCGAAAGAGAGCTGAGTGGTCTGCGCAC	828				
Qy	556	CGCTGAGCAATACTAGCATAAACCCCTTTGGGGCTCTAAACGGGTCTTTGAGGGGTTTTT	615				
Db	829	CGCTGAGCAATACTAGCATAAACCCCTTTGGGGCTCTAAACGGGTCTTTGAGGGGTTTTT	888				
Qy	616	GCTGAAGAGGAACTATATCCGGATGACCTGCGAGGCAAGCTCTAGAAATCGATACGATTT	675				
Db	889	GCTGAAGAGGAACTATATCCGGATGACCTGCGAGGCAAGCTCTAGAAATCGATACGATTT	948				
Qy	676	TGAAGTGGCAACAGATATAAAGAGAGCTTTAAATTTGTTGCTCAACTTTTAAACCAAGC	735				
Db	949	TGAAGTGGCAACAGATATAAAGAGAGCTTTAAATTTGTTGCTCAACTTTTAAACCAAGC	1008				
Qy	736	AAATACAAATCATTTGTCGAACAGATAGCGACAGAGAGGCGAAACATTTGCTGTCGAT	795				
Db	1009	AAATACAAATCATTTGTCGAACAGATAGCGACAGAGAGGCGAAACATTTGCTGTCGAT	1068				
Qy	796	CATTATAAGCAATCGCTTTCTTAAGATATAACGTTATAAGAGCTATGGATCAATAG	855				
Db	1069	CATTATAAGCAATCGCTTTCTTAAGATATAACGTTATAAGAGCTATGGATCAATAG	1128				
Qy	856	TTTAGAAAAAGATGTGATCCGTAGCGGTTTCAAAATTTGCAACAGAGATGAATTAATA	915				
Db	1129	TTTAGAAAAAGATGTGATCCGTAGCGGTTTCAAAATTTGCAACAGAGATGAATTAATA	1188				
Qy	916	TCCCTTTTATCAAGAGCGGCAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAA	975				
Db	1189	TCCCTTTTATCAAGAGCGGCAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAA	1248				
Qy	976	GATATAATGGAGATAGACGGTTTCGTTGCTGCTGACCTGACCTGACCAATATCAATAATC	1035				
Db	1249	GATATAATGGAGATAGACGGTTTCGTTGCTGCTGACCTGACCTGACCAATATCAATAATC	1308				
Qy	1036	GAACAGCAAGAAATCGCGAAACGTAAGAAAAAGTTATGAAATTAAGACTTAGAAGCAAA	1095				
Db	1309	GAACAGCAAGAAATCGCGAAACGTAAGAAAAAGTTATGAAATTAAGACTTAGAAGCAAA	1368				
Qy	1096	CTTAAGAGTGTGTAGTATGAGTATCTTAAATTTTGTATTAATAGGATTTGAAGTTAA	1155				
Db	1369	CTTAAGAGTGTGTAGTATGAGTATCTTAAATTTTGTATTAATAGGATTTGAAGTTAA	1428				
Qy	1156	ATTAGATGCTAAAAATTTGTAATTAAGAGGAGTGATTACATGAACAAAAATATAAATA	1215				
Db	1429	ATTAGATGCTAAAAATTTGTAATTAAGAGGAGTGATTACATGAACAAAAATATAAATA	1488				
Qy	1216	TTCTCAAAAATTTTAAAGAGTGAAAGAACTCAACCAAAATTAATAAACAATTTGAATTT	1275				
Db	1489	TTCTCAAAAATTTTAAAGAGTGAAAGAACTCAACCAAAATTAATAAACAATTTGAATTT	1548				
Qy	1276	AAAGAAACCGATACCGTTTACGAAATTTGGAACAGGTAAAGGCACTTTAAGCAGAACT	1335				
Db	1549	AAAGAAACCGATACCGTTTACGAAATTTGGAACAGGTAAAGGCACTTTAAGCAGAACT	1608				
Qy	1336	GGCTAAATAAGTAAACAGGTAAAGTATTTGAATTTAGACAGTCACTATTTCAACTATC	1395				
Db	1609	GGCTAAATAAGTAAACAGGTAAAGTATTTGAATTTAGACAGTCACTATTTCAACTATC	1668				
Qy	1396	GTCAAGAAATTAAGAACTGATCTCGTGTCACTTTAAATTTTCAACAGATATTTCAAGTT	1455				
Db	1669	GTCAAGAAATTAAGAACTGATCTCGTGTCACTTTAAATTTTCAACAGATATTTCAAGTT	1728				
Qy	1456	TCAATTCCTTCAACAAACAGAGGTATAAATTTTGGAGTATTTCCCTTACCATTTAAGCAC	1515				
Db	1729	TCAATTCCTTCAACAAACAGAGGTATAAATTTTGGAGTATTTCCCTTACCATTTAAGCAC	1788				

Qy	1516	ACAAATTTATTAATAAAGTGGTTTTTGAAGCCATCGCTGTGACATCTATCTGATTGTGA	1575				
Db	1789	ACAAATTTATTAATAAAGTGGTTTTTGAAGCCATCGCTGTGACATCTATCTGATTGTGA	1848				
Qy	1576	AGAAGATTTCTACAAGCGTACCTTGGATATTCACCGAACATAGGGTGTCTTTCACAC	1635				
Db	1849	AGAAGATTTCTACAAGCGTACCTTGGATATTCACCGAACATAGGGTGTCTTTCACAC	1908				
Qy	1636	TCAAGTCTCGATTTCAGCAATTCCTTAAGCTGCCAGGAATGCTTTTCATCTCTAAACCAA	1695				
Db	1909	TCAAGTCTCGATTTCAGCAATTCCTTAAGCTGCCAGGAATGCTTTTCATCTCTAAACCAA	1968				
Qy	1696	AGTAAACAGTGTCTTAATAAATTAACCTTACCGCCATACCAAGATGTTCCAGATAATTTG	1755				
Db	1969	AGTAAACAGTGTCTTAATAAATTAACCTTACCGCCATACCAAGATGTTCCAGATAATTTG	2028				
Qy	1756	GAACTATATACGTACTTTGTTTCAAAATGGGTCAATCGAGAATTCGTCAACTGTTTAC	1815				
Db	2029	GAACTATATACGTACTTTGTTTCAAAATGGGTCAATCGAGAATTCGTCAACTGTTTAC	2088				
Qy	1816	TAAATCAGTTCATCAAGCAATGAACACGCCAAAGTAAACAAATTTAAGTACCGTTTAC	1875				
Db	2089	TAAATCAGTTCATCAAGCAATGAACACGCCAAAGTAAACAAATTTAAGTACCGTTTAC	2148				
Qy	1876	TTATGAGCAATTTGTTCTATTTTAAATGTTTCTATTTTAAAGTACCGGAGGAAATAAT	1935				
Db	2149	TTATGAGCAATTTGTTCTATTTTAAATGTTTCTATTTTAAAGTACCGGAGGAAATAAT	2208				
Qy	1936	CTATGAGTCCGTTTTGTAATTTGAAATTTACAGTTTACAGTTTAAAGGGAATGAGATAAT	1995				
Db	2209	CTATGAGTCCGTTTTGTAATTTGAAATTTACAGTTTACAGTTTAAAGGGAATGAGATAAT	2268				
Qy	1996	TATTAGGTATATCTAGCAGCTTCCAAAGGAGCTTAAAGAGTCCCTAGCGTCTTTATCAT	2055				
Db	2269	TATTAGGTATATCTAGCAGCTTCCAAAGGAGCTTAAAGAGTCCCTAGCGTCTTTATCAT	2328				
Qy	2056	GGGAGAGTCCGATCATATGCAAGCAAAATAAACTCGCAACAGCACTTGGAGAAATGGG	2115				
Db	2329	GGGAGAGTCCGATCATATGCAAGCAAAATAAACTCGCAACAGCACTTGGAGAAATGGG	2388				
Qy	2116	ACGAATCGAGAAAAACCTTTTACGCTGGATTACATATCTAATAAGCCGTAAGAGAGC	2175				
Db	2389	ACGAATCGAGAAAAACCTTTTACGCTGGATTACATATCTAATAAGCCGTAAGAGAGC	2448				
Qy	2176	GGTTCAAAAAGTTTTAAATTAAGGAGAGCAATCAATGCATTTAGCTAGAACTATATTTT	2235				
Db	2449	GGTTCAAAAAGTTTTAAATTAAGGAGAGCAATCAATGCATTTAGCTAGAACTATATTTT	2508				
Qy	2236	TGGACAACTGAGAAATTTAGAGAACGTCCTCTCCAGACCAAGTTTCAAGAGCTTAGTGC	2295				
Db	2509	TGGACAACTGAGAAATTTAGAGAACGTCCTCTCCAGACCAAGTTTCAAGAGCTTAGTGC	2568				
Qy	2296	ACTAAACATTAATTAACGCTTAAGTGTGTGGAACTGTATATATATGGAAAAAGCCGT	2355				
Db	2569	ACTAAACATTAATTAACGCTTAAGTGTGTGGAACTGTATATATATGGAAAAAGCCGT	2628				
Qy	2356	AGAAATTTAAAGCAAGAGAGGAAATTTAGAGAGATTTAATGCCATATGCGTCCGCTT	2415				
Db	2629	AGAAATTTAAAGCAAGAGAGGAAATTTAGAGAGATTTAATGCCATATGCGTCCGCTT	2688				
Qy	2416	AGGATGGGAACATATCAATTTTCTGGGAATAAATAATTTCAAGGATTTACATGACATGG	2475				
Db	2689	AGGATGGGAACATATCAATTTTCTGGGAATAAATAATTTCAAGGATTTACATGACATGG	2748				
Qy	2476	GCATAATGAATTTACGTCCTTTTACGTATATAAAGAGCCGTTTTTCTTTAATATACGGCTC	2535				
Db	2749	GCATAATGAATTTACGTCCTTTTACGTATATAAAGAGCCGTTTTTCTTTAATATACGGCTC	2808				
Qy	2536	TTTTTATAGAAAAATTCCTTAGCGTGGTTTTTTTTCCGAAATGCTGGCGGTACCCCAAGAA	2595				
Db	2809	TTTTTATAGAAAAATTCCTTAGCGTGGTTTTTTTTCCGAAATGCTGGCGGTACCCCAAGAA	2868				
Qy	2596	TTAGAAATGAGTAGTCAATTTATTCAGAAATAGAAATCAGAAATCAGATCCCAACATA	2655				

Db 2869 TTAGNAATGAGTAGATCAATTAATTCAGGAATAGAAATCAGAAATCAGATCCAAACCAT 2928
QY 2656 AAAACACTAGAACAAATTTGCAAGTTAACTAACTCAACGGTAGTAGTGGATTTAATCCCA 2715
Db 2929 AAAACACTAGAACAAATTTGCAAGTTAACTAACTCAACGGTAGTAGTGGATTTAATCCCA 2988
QY 2716 AATGAGCCAAACAGAACCCAGAGCCAGAACAGAAATCAGAACAGTAACATTTGGATTAGAA 2775
Db 2989 AATGAGCCAAACAGAACCCAGAGCCAGAACAGAAATCAGAACAGTAACATTTGGATTAGAA 3048
QY 2776 ATGGAAGAAAGAAAAGCAATGACTTGTGTGAATAATGCAACGAAATCGTTGCTTATTTT 2835
Db 3049 ATGGAAGAAAGAAAAGCAATGACTTGTGTGAATAATGCAACGAAATCGTTGCTTATTTT 3108
QY 2836 TTTTAAAGCGGTATCTAGATATACGAACCAACCACTGAATAGAAACGAAAGAAAGA 2895
Db 3109 TTTTAAAGCGGTATCTAGATATACGAACCAACCACTGAATAGAAACGAAAGAAAGA 3168
QY 2896 GCCATGACACATTTATAAAATGTTTGACGACATTTTATAATGCATAGCCCGATPAAGATT 2955
Db 3169 GCCATGACACATTTATAAAATGTTTGACGACATTTTATAATGCATAGCCCGATPAAGATT 3228
QY 2956 GCCAAACCAACGCTTATCAGTTAGTCAGATGAACCTCTCCCTCGTAGAAGTTATTTAAT 3015
Db 3229 GCCAAACCAACGCTTATCAGTTAGTCAGATGAACCTCTCCCTCGTAGAAGTTATTTAAT 3288
QY 3016 TAACTTTGTTGAACGCGTATATAACCGTACTATCAATTATATAGGGAATCAGAGAGTT 3075
Db 3289 TAACTTTGTTGAACGCGTATATAACCGTACTATCAATTATATAGGGAATCAGAGAGTT 3348
QY 3076 TTCAGATCTAAGCTACTGAATTTAAGATTTGTTAAGCAATCAATCGGAAATCGTTTGA 3135
Db 3349 TTCAGATCTAAGCTACTGAATTTAAGATTTGTTAAGCAATCAATCGGAAATCGTTTGA 3408
QY 3136 TTGCTTTTTTTGTTATTCATTTATAGAGTGAGTTGTTGTAATGAATCATGATGAATGTAAA 3195
Db 3409 TTGCTTTTTTTGTTATTCATTTATAGAGTGAGTTGTTGTAATGAATCATGATGAATGTAAA 3468
QY 3196 ACTTATATAAAATPAGTTTATTTGAGATAGAAATTTAGCAATATCTATACACTAGAA 3255
Db 3469 ACTTATATAAAATPAGTTTATTTGAGATAGAAATTTAGCAATATCTATACACTAGAA 3528
QY 3256 AGTTTAAAGAGTTTAAAGAGTAATCTACTTAGAACAATAATCAGATAAGTAT 3315
Db 3529 AGTTTAAAGAGTTTAAAGAGTAATCTACTTAGAACAATAATCAGATAAGTAT 3588
QY 3316 TTTTCTTCGGAGGGGAGATTTATATATAGTTTAAATAGAAAATAACAAATAATTTAT 3375
Db 3589 TTTTCTTCGGAGGGGAGATTTATATATAGTTTAAATAGAAAATAACAAATAATTTAT 3648
QY 3376 TCGATTAGTGGAAAATTTGACTTATTAAGGAAAATCTTTTCAAAATGCAATA 3435
Db 3649 TCGATTAGTGGAAAATTTGACTTATTAAGGAAAATCTTTTCAAAATGCAATA 3708
QY 3436 TTGAAACAGTTGAATGAAAAGCAACCAAGTTAATTAACAACTATTTTATAGGATTT 3495
Db 3709 TTGAAACAGTTGAATGAAAAGCAACCAAGTTAATTAACAACTATTTTATAGGATTT 3768
QY 3496 ATAGAAAGGAGAAACAGCTGAATGAATATCCCTTTTGTGTAGAAAATGTCCTTCATGAC 3555
Db 3769 ATAGAAAGGAGAAACAGCTGAATGAATATCCCTTTTGTGTAGAAAATGTCCTTCATGAC 3828
QY 3556 GGCCTTTTAAAGTACAAATTTTAAATAATAGTAAATTCGCTCAATCACTACCAGCCAGGT 3615
Db 3829 GGCCTTTTAAAGTACAAATTTTAAATAATAGTAAATTCGCTCAATCACTACCAGCCAGGT 3888
QY 3616 AAAAGCAAGGGGCTATTTTTCGCTATCGCTCAAAATCAAGCATGATTTGGCGGTCGTGGT 3675
Db 3889 AAAAGCAAGGGGCTATTTTTCGCTATCGCTCAAAATCAAGCATGATTTGGCGGTCGTGGT 3948
QY 3676 GTTGTCTGACCTCCGAGGAGCGATTCAAGAAATCAAGATACATTTACATTTGGACA 3735

Db 3949 GTTGTCTGACCTCCGAGGAAGCGATTCAAGAAAATCAAGATACATTTACACATTGGACA 4008
QY 3736 CCCAACGTTTATCGTTATTTGGAACGATATCAGACGAAAACCGTTTATACACGAAAAGGACAT 3795
Db 4009 CCCAACGTTTATCGTTATTTGGAACGATATCAGACGAAAACCGTTTATACACGAAAAGGACAT 4068
QY 3796 TCTGAAAACAAATTTAAGACAAATCAATACCTTTCTTTTATTTGATTTTGTATTTTCAACGGCA 3855
Db 4069 TCTGAAAACAAATTTAAGACAAATCAATACCTTTCTTTTATTTGATTTTGTATTTTCAACGGCA 4128
QY 3856 AAAGAACTATTTTCAGCAAGCGATATTTTAAACACCGCTATTTGATTTAGGTTTATGGCT 3915
Db 4129 AAAGAACTATTTTCAGCAAGCGATATTTTAAACACCGCTATTTGATTTAGGTTTATGGCT 4188
QY 3916 ACTATGATTATCAAACTCTGATAAAGGTTATCAAGCATATTTTGTTTTGAACCGCAGTC 3975
Db 4189 ACTATGATTATCAAACTCTGATAAAGGTTATCAAGCATATTTTGTTTTGAACCGCAGTC 4248
QY 3976 TATGTGACTTCAAAATCAGAAATTTAAATCTCTCAAGCAGCAAAATAATTTTCGCAAAAT 4035
Db 4249 TATGTGACTTCAAAATCAGAAATTTAAATCTCTCAAGCAGCAAAATAATTTTCGCAAAAT 4308
QY 4036 ATCCGAGAAATATTTTGGAAAGTCTTTGCGAGTTGATCTAAACGCTGTAATCATTTTGGTAT 4095
Db 4309 ATCCGAGAAATATTTTGGAAAGTCTTTGCGAGTTGATCTAAACGCTGTAATCATTTTGGTAT 4368
QY 4096 GTCGCTATCAAGAACCGACCAATGTAGAAATTTTGTGATCTTAATACCGTTATTTCTTC 4155
Db 4369 GTCGCTATCAAGAACCGACCAATGTAGAAATTTTGTGATCTTAATACCGTTATTTCTTC 4428
QY 4156 AAAGAAATGCAAGATTTGTTCTTTTCAACAAACAGATAATTAAGGGCTTTACTCGTTCAAGT 4215
Db 4429 AAAGAAATGCAAGATTTGTTCTTTTCAACAAACAGATAATTAAGGGCTTTACTCGTTCAAGT 4488
QY 4216 CTACCGTTTTAAGCGGTACAGAGCGCAAAACAAAGTAGTAGAAACCTCGTTTAAATCTC 4275
Db 4489 CTACCGTTTTAAGCGGTACAGAGCGCAAAACAAAGTAGTAGAAACCTCGTTTAAATCTC 4548
QY 4276 TTATTTGCAAGAACGAAATTTTTCAGGAGAAAGGGTTTAAATAGGGCTTAAATAACGTCATG 4335
Db 4549 TTATTTGCAAGAACGAAATTTTTCAGGAGAAAGGGTTTAAATAGGGCTTAAATAACGTCATG 4608
QY 4336 TTATACCTCTCTTTAGCCCTACTTTTAGTTTCAAGCTATTCAATCGAAACCGTGGAAATTAAT 4395
Db 4609 TTATACCTCTCTTTAGCCCTACTTTTAGTTTCAAGCTATTCAATCGAAACCGTGGAAATTAAT 4668
QY 4396 ATGTTTGAGTTTAAATATCGATTAGATCAACCTTTAGAGAAAAGAGTAGTAATCAAAAT 4455
Db 4669 ATGTTTGAGTTTAAATATCGATTAGATCAACCTTTAGAGAAAAGAGTAGTAATCAAAAT 4728
QY 4456 GTTAGAAGTGCCTATTTCAGAAAACCTATCAAGGGGCTAATAGGGAATACATACCAATCTT 4515
Db 4729 GTTAGAAGTGCCTATTTCAGAAAACCTATCAAGGGGCTAATAGGGAATACATACCAATCTT 4788
QY 4516 TGCAAGCTTTGGGTATCAAGTGAATTTAACAGTAAGATTTTATTTGTCGGTCAAGGGTGG 4575
Db 4789 TGCAAGCTTTGGGTATCAAGTGAATTTAACAGTAAGATTTTATTTGTCGGTCAAGGGTGG 4848
QY 4576 TTTAAATTCAGAAAAGAGAGCGAAACGTCCTCAACGTTTCAATTTCTCAGAAATGGAAGAA 4635
Db 4849 TTTAAATTCAGAAAAGAGAGCGAAACGTCCTCAACGTTTCAATTTCTCAGAAATGGAAGAA 4908
QY 4636 GATTTAATGGCTTATTTAGCGAAAAGAGCGATGTATACAGCCCTATTTAGTGCAGCC 4695
Db 4909 GATTTAATGGCTTATTTAGCGAAAAGAGCGATGTATACAGCCCTATTTAGTGCAGCC 4968
QY 4696 AAAAAGAGATTAGAGAGTGTCTAGCATTTCTGAAACGACATTAGATAAATTTGCTGAAG 4755
Db 4969 AAAAAGAGATTAGAGAGTGTCTAGCATTTCTGAAACGACATTAGATAAATTTGCTGAAG 5028
QY 4756 GTACTGAAGCGGAATCAGGAAATTTTCTTTAAGATTAAACCCAGGAAGAAATCGTGGCAT 4815
Db 5029 GTACTGAAGCGGAATCAGGAAATTTTCTTTAAGATTAAACCCAGGAAGAAATCGTGGCAT 5088

QY	1095	ACTTAAGAGTGTGTGATGCGATCTTAAATTTTGTATATAAGGAATTTGAAGTTA	1154	QY	2175	GGTTTCAAAAAGGTTTAAATTAAGGAGAACCAATCAATGCATTAGCTAGACTATATTTT	2234
Db	1504	ACTTAAGAGTGTGTGATGCGATCTTAAATTTTGTATATAAGGAATTTGAAGTTA	1563	Db	2584	GGTTTCAAAAAGGTTTAAATTAAGGAGAACCAATCAATGCATTAGCTAGACTATATTTT	2643
QY	1155	AATTAGATGCTTAAAAATTTGTAAATTAAGAAGGAGTGATTCATGAACAAAAATATAAAT	1214	QY	2235	TTGGACACGCTGGAGAAATTTAGAGAACGTCCTCCAAAGACCACTTACAAAGAGCTAGTG	2294
Db	1564	AATTAGATGCTTAAAAATTTGTAAATTAAGAAGGAGTGATTCATGAACAAAAATATAAAT	1623	Db	2644	TTGGACACGCTGGAGAAATTTAGAGAACGTCCTCCAAAGACCACTTACAAAGAGCTAGTG	2703
QY	1215	ATTCTCAAACTTTTAAACGAGTGAAAGAGTACTCAACCAAAATATAAACAATTTGAAT	1274	QY	2295	CACTAAAACATTAATTAACGCTATAGTGTGTGGACACACTGTATATATGAAAAAAGCCG	2354
Db	1624	ATTCTCAAACTTTTAAACGAGTGAAAGAGTACTCAACCAAAATATAAACAATTTGAAT	1683	Db	2704	CACTAAAACATTAATTAACGCTATAGTGTGTGGACACACTGTATATATGAAAAAAGCCG	2763
QY	1275	TAAAGAAACCGATACACGTTTACGAAATTTGAAACAGGTAAAGGCACTTTAACGACGAAC	1334	QY	2355	TAGAGAAATTAAGCAAGAGAGAGAAATTTAGAGAAATTTAATGCCATATCGCTGGCGGT	2414
Db	1684	TAAAGAAACCGATACACGTTTACGAAATTTGAAACAGGTAAAGGCACTTTAACGACGAAC	1743	Db	2764	TAGAGAAATTAAGCAAGAGAGAGAAATTTAGAGAAATTTAATGCCATATCGCTGGCGGT	2823
QY	1335	TGGCTAAATTAAGTAACAGGTAACGTTATTTGAATTTAGACAGTCACTATTCAACTTAT	1394	QY	2415	TAGGATGGGAACATATCAATTTTCTTGAGAAATACAAATTTGAAGGATTAATGACACTG	2474
Db	1744	TGGCTAAATTAAGTAACAGGTAACGTTATTTGAATTTAGACAGTCACTATTCAACTTAT	1803	Db	2824	TAGGATGGGAACATATCAATTTTCTTGAGAAATACAAATTTGAAGGATTAATGACACTG	2883
QY	1395	CGTCAGAAAAATTAACACTGAATCTCGTGCACTTTAATTCACCAAGATATTTCTACAGT	1454	QY	2475	GCCTAATGAATTTACGTCCTTTACGTATAAAGAGCCGTTTTTATTCTTAAATATAACGGCT	2534
Db	1804	CGTCAGAAAAATTAACACTGAATCTCGTGCACTTTAATTCACCAAGATATTTCTACAGT	1863	Db	2884	GCCTAATGAATTTACGTCCTTTACGTATAAAGAGCCGTTTTTATTCTTAAATATAACGGCT	2943
QY	1455	TTCAATCCCTAACAAACAGAGGTATAAATTTGTGGAGTATTCCTTCAATTAAGCA	1514	QY	2535	CTTTTATAGAAAAAATCTTAGCGTGTGTTTTTTCGAAATGCTGGCGGTACCCCAAGA	2594
Db	1864	TTCAATCCCTAACAAACAGAGGTATAAATTTGTGGAGTATTCCTTCAATTAAGCA	1923	Db	2944	CTTTTATAGAAAAAATCTTAGCGTGTGTTTTTTCGAAATGCTGGCGGTACCCCAAGA	3003
QY	1515	CACAAATTAATAAAGAGTGTGTTTGAAGCCATGCTCTGACATCTATCTGATTTGTTG	1574	QY	2595	ATTAGAAATGAGTAGATCAATTTTACGTAATAAGAGCCGTTTTTATTCTTAAATATAACGGCT	2654
Db	1924	CACAAATTAATAAAGAGTGTGTTTGAAGCCATGCTCTGACATCTATCTGATTTGTTG	1983	Db	3004	ATTAGAAATGAGTAGATCAATTTTACGTAATAAGAGCCGTTTTTATTCTTAAATATAACGGCT	3063
QY	1575	AAGAAGGATTTCAAGCGTACCTTGGATATTCACCGAACACTAGGTTGCTCTTGCA	1634	QY	2655	AAAAACACTAGAACAAATGCAAGCTTAACTCAACGCTAGTAGTGGATTTAATCCC	2714
Db	1984	AAGAAGGATTTCAAGCGTACCTTGGATATTCACCGAACACTAGGTTGCTCTTGCA	2043	Db	3064	AAAAACACTAGAACAAATGCAAGCTTAACTCAACGCTAGTAGTGGATTTAATCCC	3123
QY	1635	CTCAAGTCTGATTCAGCAATGCTTAAGCTGCCAGCGGATGCTTTCATCCTTAAACCA	1694	QY	2715	AAATGAGCCAAACAGAACCCAGAGCCAGAACCAAGATCAGAACCAAGTAACTTGGATTTAGA	2774
Db	2044	CTCAAGTCTGATTCAGCAATGCTTAAGCTGCCAGCGGATGCTTTCATCCTTAAACCA	2103	Db	3124	AAATGAGCCAAACAGAACCCAGAGCCAGAACCAAGATCAGAACCAAGTAACTTGGATTTAGA	3183
QY	1695	AAGTAAACAGTCTCTTAATAAACTTACCCGCCATACCAACAGATGTTTCCAGATAAATTT	1754	QY	2775	AATGGAAGAGAAAAAAGCAATGACTCTGTGTAATTAATGACGAAATCGTTGCTTATTT	2834
Db	2104	AAGTAAACAGTCTCTTAATAAACTTACCCGCCATACCAACAGATGTTTCCAGATAAATTT	2163	Db	3184	AATGGAAGAGAAAAAAGCAATGACTCTGTGTAATTAATGACGAAATCGTTGCTTATTT	3243
QY	1755	GGAAGCTATACGTCTTGTGTTTCAAAATGGGTCATTCGAGATATCGTCACTGTTTA	1814	QY	2835	TTTTTTAAAGGCGGTATCTAGATATAACGAAACCAACGAACTGAATAGAACCAAAAAG	2894
Db	2164	GGAAGCTATACGTCTTGTGTTTCAAAATGGGTCATTCGAGATATCGTCACTGTTTA	2223	Db	3244	TTTTTTAAAGGCGGTATCTAGATATAACGAAACCAACGAACTGAATAGAACCAAAAAG	3303
QY	1815	CTAAAAACAGTTTCATCAAGCAATGAACACCGCCAAAGTAAACAAATTTAAGTACCGTTA	1874	QY	2895	AGCCATGACACATTTTAAATTAAGTAACTTGAATTAATGATAGCCGATAAGAT	2954
Db	2224	CTAAAAACAGTTTCATCAAGCAATGAACACCGCCAAAGTAAACAAATTTAAGTACCGTTA	2283	Db	3304	AGCCATGACACATTTTAAATTAAGTAACTTGAATTAATGATAGCCGATAAGAT	3363
QY	1875	CTTATGAGCAAGTATGCTATTTTAAATAGTATCTATTTTAAACGGAGGAATTAAT	1934	QY	2955	TGCAAAACCAACGCTTATCAGTTAGTACGATGAATCTTCCCTCGTAAGAGTATTTAA	3014
Db	2284	CTTATGAGCAAGTATGCTATTTTAAATAGTATCTATTTTAAACGGAGGAATTAAT	2343	Db	3364	TGCAAAACCAACGCTTATCAGTTAGTACGATGAATCTTCCCTCGTAAGAGTATTTAA	3423
QY	1935	TCTATGAGTCTGTTTGTAAATTTGAAAGTTTACAGTTTCTTAAAGGGAATGTAGATAAA	1994	QY	3015	TTAACTTTGTTTGAAGACCGGTATTAACCGTACTATTAACCGTACTATTAATAGGGAATTCAGAGAGT	3074
Db	2344	TCTATGAGTCTGTTTGTAAATTTGAAAGTTTACAGTTTCTTAAAGGGAATGTAGATAAA	2403	Db	3424	TTAACTTTGTTTGAAGACCGGTATTAACCGTACTATTAACCGTACTATTAATAGGGAATTCAGAGAGT	3483
QY	1995	TTATTAGGTATCTACTGACAGCTTCCAAGGAGCTTAAAGAGTCCCTTAGCGCTCTTATCA	2054	QY	3075	TTTCAAGTATCTAAGCTACTGAAATTTAAGAAATTTGTTAAGCAATCAATCGGAATCGTTTG	3134
Db	2404	TTATTAGGTATCTACTGACAGCTTCCAAGGAGCTTAAAGAGTCCCTTAGCGCTCTTATCA	2463	Db	3484	TTTCAAGTATCTAAGCTACTGAAATTTAAGAAATTTGTTAAGCAATCAATCGGAATCGTTTG	3543
QY	2055	TGGGAGAGCTCCGATCATATGCAAGCAAAATAAATCGCAACAGCACTTGGAGAAATGG	2114	QY	3135	ATTGCTTTTTTTGTATTCATTTATAGAGGAGTGTGTTGTTGTAATCATGATGAATGTAA	3194
Db	2464	TGGGAGAGCTCCGATCATATGCAAGCAAAATAAATCGCAACAGCACTTGGAGAAATGG	2523	Db	3544	ATTGCTTTTTTTGTATTCATTTATAGAGGAGTGTGTTGTTGTAATCATGATGAATGTAA	3603
QY	2115	GACGAATCGAGAAAACCCCTCTTTAGCTGGATTACATATCTAATAAAGCCGTAAGAGAC	2174	QY	3195	AACTTATATAAAAAATAGTTTTTATGGAGATAGAAAAATTTAGCAAAATATCTATACACTAGA	3254
Db	2524	GACGAATCGAGAAAACCCCTCTTTAGCTGGATTACATATCTAATAAAGCCGTAAGAGAC	2583	Db	3604	AACTTATATAAAAAATAGTTTTTATGGAGATAGAAAAATTTAGCAAAATATCTATACACTAGA	3663
				QY	3255	AACGTTTAAAGAAAGGTTTAGAAAAAGAAATATCTACTTTAGAAACAAAAATCAGATAAGTA	3314

Db 3664 AACGTTTAAAGAAAGAGTTAGAAAAGAGAAATATCTACTTAGAAACAAATCAGATAAGTA 3723
QY 3315 TTTTCTTCGAGGGGAAAGATATATATATAGCTTAATAGAAATAACAAATAATTTTA 3374
Db 3724 TTTTCTTCGAGGGGAGATATATATATAGCTTAATAGAAATAACAAATAATTTTA 3783
QY 3375 TCTGATTAGTGGAAAAAATGACTTATAAGGAAAAAATCTTTTCAAAACATGCAAT 3434
Db 3784 TTCGATTAGTGGAAAAAATGACTTATAAGGAAAAAATCTTTTCAAAACATGCAAT 3843
QY 3435 ATTCAAAACAGTTGAATCAAAAAGCAACCAAGTTAATTAACACACCTATTATTAGGATT 3494
Db 3844 ATTGAACAGTTGATCGAAAGCAACCAAGTTAATTAACACACCTATTATTAGGATT 3903
QY 3495 TATAGAAAGAGAAACAGCTGAATGAATATCCCTTTTGTGTAGAAACCTGTGCTTCATGA 3554
Db 3904 TATAGAAAGAGAAACAGCTGAATGAATATCCCTTTTGTGTAGAAACCTGTGCTTCATGA 3963
QY 3555 CGGCTTCTTAAGTACAAATTTAAATAAGTAAATTCGCTCAATCACTACCAAGCCAGG 3614
Db 3964 CGGCTTCTTAAGTACAAATTTAAATAAGTAAATTCGCTCAATCACTACCAAGCCAGG 4023
QY 3615 TAAAGCAAAAGGGGCTATTTTTCGCTATCGCTCAAAATCAAGCATGATTGGCGGTCGTGG 3674
Db 4024 TAAAGCAAAAGGGGCTATTTTTCGCTATCGCTCAAAATCAAGCATGATTGGCGGTCGTGG 4083
QY 3675 TGTGTTCTGACTTCGAGGAAGCGATTCAAGAAATCAAGATACATTTACACATTTGGAC 3734
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QY 3735 ACCCAAGCTTTATCGTTATGGAACGTTATGCAGACGAAACCGTTTCATACAGAAAGGACA 3794
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QY 3855 AAAAGAAACCTATTCAGACAGCGATATTTTAAACACCGCTATTGATTTAGGTTTATGCC 3914
Db 4264 AAAAGAAACCTATTCAGACAGCGATATTTTAAACACCGCTATTGATTTAGGTTTATGCC 4323
QY 3915 TACTATGATTATCAAAATCTGATAAAGGTTATCAAGCATATTTTGTGTTTGAACCGCCAGT 3974
Db 4324 TACTATGATTATCAAAATCTGATAAAGGTTATCAAGCATATTTTGTGTTTGAACCGCCAGT 4383
QY 3975 CTATGTCGACTTCAAAATCAGAAATTTAAATCTGTCAGACGACCAAAATTTTCGCAAAA 4034
Db 4384 CTATGTCGACTTCAAAATCAGAAATTTAAATCTGTCAGACGACCAAAATTTTCGCAAAA 4443
QY 4035 TATCCGAGATATTTTGGAAAGTCTTTGCCAGTTGATCTAACGTGTAATCATTTTCGGTAT 4094
Db 4444 TATCCGAGATATTTTGGAAAGTCTTTGCCAGTTGATCTAACGTGTAATCATTTTCGGTAT 4503
QY 4095 TGCTCGCATACCAAGAACGACAAATGTAGAAATTTTGTGATCTCTTAATTCGTTATCTTT 4154
Db 4504 TGCTCGCATACCAAGAACGACAAATGTAGAAATTTTGTGATCTCTTAATTCGTTATCTTT 4563
QY 4155 CAAAGAAATGCAAGATTTGCTTTTCAAAACAAACAGATTAATAGGGGCTTTTACTCGTTCAAG 4214
Db 4564 CAAAGAAATGCAAGATTTGCTTTTCAAAACAAACAGATTAATAGGGGCTTTTACTCGTTCAAG 4623
QY 4215 TCTAAACGGTTTAAAGCGGTAACAGAGGCAAAACCAAGTAGATGAACCCCTGGTTTAACTC 4274
Db 4624 TCTAAACGGTTTAAAGCGGTAACAGAGGCAAAACCAAGTAGATGAACCCCTGGTTTAACTC 4683
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Db 4684 CTTATTGCAAGAACGAAATTTTCAGAGAAAGGGTTTAAATAGGCGGTAATAACGTCAT 4743
QY 4335 GTTTACCTCTCTTTAGCCCTACTTTTAGTTTCAAGCTATTCOAATCGAAACGTCGGAATATAA 4394

Db 4744 GTTTACCTCTCTTTAGCCCTACTTTTAGTTCAAGCTATTCAATCGAAACGTCGGAATATAA 4803
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QY 4515 TTGCAAGCTTGGGTATCAAGTGATTAAACGATTAAGATTTATTTGTCGTCGCAAGGGTG 4574
Db 4924 TTGCAAGCTTGGGTATCAAGTGATTAAACGATTAAGATTTATTTGTCGTCGCAAGGGTG 4983
QY 4575 GTTTAAATTCAGAAAAAAGAAAGCGTCAACGCTGTTTCATTGTCAGAAATGAAAGA 4634
Db 4984 GTTTAAATTCAGAAAAAAGAAAGCGTCAACGCTGTTTCATTGTCAGAAATGAAAGA 5043
QY 4635 AGATTTAATGCTTATATTAGGAAAAAAGCGATGTATACAGCCCTTATTTAGTGACGAC 4694
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QY 4695 CAAAAAGAGATTAGAGAAAGTGTAGGCAATTCCTGAACGGACATTAGATAAATTCCTCAA 4754
Db 5104 CAAAAAGAGATTAGAGAAAGTGTAGGCAATTCCTGAACGGACATTAGATAAATTCCTCAA 5163
QY 4755 GGTACTGAAGGCGAATTCAGAAATTTTCTTAAAGATTAACCAAGAAAGATGCTGGCAT 4814
Db 5164 GGTACTGAAGGCGAATTCAGAAATTTTCTTAAAGATTAACCAAGAAAGATGCTGGCAT 5223
QY 4815 TCACCTGCTAGTGTAAATCATTTGCTGCTATCGATTCATTAAGTAAAGTAAAGAAAGAGAAA 4874
Db 5224 TCACCTGCTAGTGTAAATCATTTGCTGCTATCGATTCATTAAGTAAAGTAAAGAAAGAGAAA 5283
QY 4875 AGAAAGCTATATAAGGCGCTGACAAATTTCTTTGACTTAGAGCATACATTCATTCAAGA 4934
Db 5284 AGAAAGCTATATAAGGCGCTGACAAATTTCTTTGACTTAGAGCATACATTCATTCAAGA 5343
QY 4935 GACTTTAAACAGCTAGCAGAACCGCCCTTAAACGGACACAACTCGATTTGTTTAGCTA 4994
Db 5344 GACTTTAAACAGCTAGCAGAACCGCCCTTAAACGGACACAACTCGATTTGTTTAGCTA 5403
QY 4995 TGATACAGCTGAAATTAACCCCGCCTATGCCATTACATTTATATCTATGATACGCTGT 5054
Db 5404 TGATACAGCTGAAATTAACCCCGCCTATGCCATTACATTTATATCTATGATACGCTGT 5463
QY 5055 TTGTTTTTTCTTGTGTTTACGGAATGATTAGCAGAAATATACAGAGTAAGATTTTAAT 5114
Db 5464 TTGTTTTTTCTTGTGTTTACGGAATGATTAGCAGAAATATACAGAGTAAGATTTTAAT 5523
QY 5115 TAAATTTATAGGGGAGAGAGAGTAGCCCGAAACCTTTTAGTTGCTTTGGACTGAAC 5174
Db 5524 TAAATTTATAGGGGAGAGAGAGTAGCCCGAAACCTTTTAGTTGCTTTGGACTGAAC 5583
QY 5175 GAAAGTGGGAAAGGCTACTAAAAACGTCGAGGGGCGTAGAGCGAAGCGAAACCTTGAT 5234
Db 5584 GAAAGTGGGAAAGGCTACTAAAAACGTCGAGGGGCGTAGAGCGAAGCGAAACCTTGAT 5643
QY 5235 TTTTAAATTTCTATCTTTTATAGTTCATTAGAGTATACATTTTGTGCTTATTAACCTATT 5294
Db 5644 TTTTAAATTTCTATCTTTTATAGTTCATTAGAGTATACATTTTGTGCTTATTAACCTATT 5703
QY 5295 TAGCAGCATATATAGATTATTGAATAGTTCATTGAATGAGCATATTAGAGGAGGAAAA 5354
Db 5704 TAGCAGCATATATAGATTATTGAATAGTTCATTGAATGAGCATATTAGAGGAGGAAAA 5763
QY 5355 TCTTGGAGAAATTTTGAAGAACCCGATTACATGGAATGGAATAGTTCTTGTGCTTACGT 5414
Db 5764 TCTTGGAGAAATTTTGAAGAACCCGATTACATGGAATGGAATAGTTCTTGTGCTTACGT 5823
QY 5415 GGTTTTTAACTAAAGTAGTGAATTTTGTGTTTGTGTTGCTGTTGTTGTTAGTAT 5474
Db 5824 GGTTTTTAACTAAAGTAGTGAATTTTGTGTTTGTGTTGCTGTTGTTGTTAGTAT 5883

QY 5475 TTGCTAGTCAAAGTGATTAAATA 5497
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DB 5884 TTGCTAGTCAAAGTGATTAAATA 5906
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RESULT 4

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992	DB	992	GAAGAGAGAACTATATCCGGATGACCTCGACGCAAGCTCTAGAAATCGATACGAATTTTCGA	105
679	QY	679	AGTGGCAACAGATAAAAAAAGCAGTTTAAAAATTGTTGCTGAACTTTTAAAAACAAGCAAA	738
1052	DB	1052	AGTGGCAACAGATAAAAAAAGCAGTTTAAAAATTGTTGCTGAACTTTTAAAAACAAGCAAA	1111
739	QY	739	TACAATCATTTGTCGCAACAGATAGCGACAGAGAAGCGCAAAACATTGCTGGTTCGATCAT	798
1112	DB	1112	TACAATCATTTGTCGCAACAGATAGCGACAGAGAAGCGCAAAACATTGCTGGTTCGATCAT	1171
799	QY	799	TCATAAAGCAAATGCCCTTTTCTAAAGATAAAACGTATATAAAGACTATGGATCAATAGTTT	858
1172	DB	1172	TCATAAAGCAAATGCCCTTTTCTAAAGATAAAACGTATATAAAGACTATGGATCAATAGTTT	1231
859	QY	859	AGAAAAAGATGTGATCCGTAGCGGTTTCCAAAAATTTCGAACAGGAATGAAATTACTATCC	918
1232	DB	1232	AGAAAAAGATGTGATCCGTAGCGGTTTCCAAAAATTTCGAACAGGAATGAAATTACTATCC	1291
919	QY	919	CTTTTATCAAGAAGCGCAAAAGAAAAAGAAATGATACACCAATCAGTCGCAAAAAAGAT	978
1292	DB	1292	CTTTTATCAAGAAGCGCAAAAGAAAAAGAAATGATACACCAATCAGTCGCAAAAAAGAT	1351
979	QY	979	ATAATGGGAGATAAGACGGTTTCGTGTCGTGACTTGGCAACATATCATAAAAATTCGAA	1038
1352	DB	1352	ATAATGGGAGATAAGACGGTTTCGTGTCGTGACTTGGCAACATATCATAAAAATTCGAA	1411
1039	QY	1039	ACGCAAAAGAAATGGCGGAAACGTTAAAAGAAAGTTATCGAAATTAAGACTTAGAACCAAACTT	1098
1412	DB	1412	ACGCAAAAGAAATGGCGGAAACGTTAAAAGAAAGTTATCGAAATTAAGACTTAGAACCAAACTT	1471
1099	QY	1099	AAGAGTGTGTGATAGTACGTATCTTAAAAATTTGTATAATAGGAATTTGAAAGTTAAAT	1158
1472	DB	1472	AAGAGTGTGTGATAGTACGTATCTTAAAAATTTGTATAATAGGAATTTGAAAGTTAAAT	1531
1159	QY	1159	AGATGCTAAAAATTTGCTTAATTAAAGAGGAGTGATACATGAACAAAAATATAAAATATTC	1218
1532	DB	1532	AGATGCTAAAAATTTGCTTAATTAAAGAGGAGTGATACATGAACAAAAATATAAAATATTC	1591
1219	QY	1219	TCAAAACTTTTTAACGAGTGA AAAAGTACTCAAACCAATATAAAAACAATTTGAATTTAAA	1278
1592	DB	1592	TCAAAACTTTTTAACGAGTGA AAAAGTACTCAAACCAATATAAAAACAATTTGAATTTAAA	1651
1279	QY	1279	AGAAAACGATACCGTTTACGAAATTCGAAACAGGTAAAGGGCATTTAACGCAAGAACTGGC	1338
1652	DB	1652	AGAAAACGATACCGTTTACGAAATTCGAAACAGGTAAAGGGCATTTAACGCAAGAACTGGC	1711
1339	QY	1339	TAAATAAGTAAACAGGTAAACGTCATTGAAATTAAGACAGTCATCTATTCAACTTATCGTC	1398
1712	DB	1712	TAAATAAGTAAACAGGTAAACGTCATTGAAATTAAGACAGTCATCTATTCAACTTATCGTC	1771
1399	QY	1399	AGAAAAATTA AAAACTCGTGTCACCTTTAAATTCACCAAGATATTTCTACAGTTTCA	1458
1772	DB	1772	AGAAAAATTA AAAACTCGTGTCACCTTTAAATTCACCAAGATATTTCTACAGTTTCA	1831
1459	QY	1459	ATTCCCTTCAAAACAGGGTATAAAAATTGTTGGAGTATTCCTTACCATTATAAGCACACA	1518
1832	DB	1832	ATTCCCTTCAAAACAGGGTATAAAAATTGTTGGAGTATTCCTTACCATTATAAGCACACA	1891
1519	QY	1519	AATTAATTA AAAAAGTGGTTTTTGAAGCCATCGGCTCGAATCTATCTGATTTGTTGAAGA	1578
1892	DB	1892	AATTAATTA AAAAAGTGGTTTTTGAAGCCATCGGCTCGAATCTATCTGATTTGTTGAAGA	1951
1579	QY	1579	AGAAATCTACAGGTTACCTTGGATATTCACCGAACACTAGGGTTGCTCTTGACACTCA	1638
1952	DB	1952	AGAAATCTACAGGTTACCTTGGATATTCACCGAACACTAGGGTTGCTCTTGACACTCA	2011
1639	QY	1639	AGTCTCGAATTCAGCAATTTGCTTAAGCTGCCAGCGGAAATGCTTTTCATCCTTAAACCAAAAGT	1698
2012	DB	2012	AGTCTCGAATTCAGCAATTTGCTTAAGCTGCCAGCGGAAATGCTTTTCATCCTTAAACCAAAAGT	2071
1699	QY	1699	AAACAGTGTCTTAATAAACTTACC CGCCATACCAAGATGTTCCAGATTAATTTGCAA	1758
2072	DB	2072	AAACAGTGTCTTAATAAACTTACC CGCCATACCAAGATGTTCCAGATTAATTTGCAA	2131

QY 1759 GCTATATACGTACTTTGTTTCAAAATCGGTCAATCGAGATATCGTCAACTGTTTACTAA 1818
DB 2132 GCTATATACGTACTTTGTTTCAAAATCGGTCAATCGAGATATCGTCAACTGTTTACTAA 2191
QY 1819 AAATCAGTTTCATCAACCAATGAACACGCGCAAGTAAACAAATTTAAGTACCGTTACTTA 1878
DB 2192 AAATCAGTTTCATCAACCAATGAACACGCGCAAGTAAACAAATTTAAGTACCGTTACTTA 2251
QY 1879 TGACCAAGTATGTCATATTTTAAATAGTTATCTATATTTAATTAACGGGAGGAAATTAATCTA 1938
DB 2252 TGACCAAGTATGTCATATTTTAAATAGTTATCTATATTTAATTAACGGGAGGAAATTAATCTA 2311
QY 1939 TGAGTCGCTTTGTTAAATTTGGAAGTTTACAGTTTACTTAAGGGAATGTAGATAAATTAAT 1998
DB 2312 TGAGTCGCTTTGTTAAATTTGGAAGTTTACAGTTTACTTAAGGGAATGTAGATAAATTAAT 2371
QY 1999 TAGGTATPACTGACAGCTTCCAGGAGCTAAAGAGTCCCTAGCGCTCTTATCATGGG 2058
DB 2372 TAGGTATPACTGACAGCTTCCAGGAGCTAAAGAGTCCCTAGCGCTCTTATCATGGG 2431
QY 2059 GAAGCTCGGATCATATCGACAGCAAAATAAATTAACCTCGCAACAGCACTTGGAGAAATGGGACG 2118
DB 2432 GAAGCTCGGATCATATCGACAGCAAAATAAATTAACCTCGCAACAGCACTTGGAGAAATGGGACG 2491
QY 2119 AATCGAGAAAACCTCTTTACGCTGGATTACATATCTAATAAAGCCGTAAAGAGACGGGT 2178
DB 2492 AATCGAGAAAACCTCTTTACGCTGGATTACATATCTAATAAAGCCGTAAAGAGACGGGT 2551
QY 2179 TCAAAAAGGTTTAAATAAAGGAGAGCAATCAATGCAATTTAGCTAGCAATATTTTTTGG 2238
DB 2552 TCAAAAAGGTTTAAATAAAGGAGAGCAATCAATGCAATTTAGCTAGCAATATTTTTTGG 2611
QY 2239 ACAAGCTGGAGAAATTTAGAGAACTGCTCTCCAAAGCCAGTTTAAAGAGCTAGTGCACCT 2298
DB 2612 ACAAGCTGGAGAAATTTAGAGAACTGCTCTCCAAAGCCAGTTTAAAGAGCTAGTGCACCT 2671
QY 2299 AAACATAATTTAAACGCTATAAGTGTGCGAACTGTTATATATGGAAGAAAGCCGTAGA 2358
DB 2672 AAACATAATTTAAACGCTATAAGTGTGCGAACTGTTATATATGGAAGAAAGCCGTAGA 2731
QY 2359 AGAATTAAGAGAGAGGAGAAATTTAGAGAAATTTAAGAGATTTAATGCCATATCGGTGGCGTTAG 2418
DB 2732 AGAATTAAGAGAGAGGAGAAATTTAGAGAAATTTAAGAGATTTAATGCCATATCGGTGGCGTTAG 2791
QY 2419 ATGGGAACATATCAATTTCTTGAGAAATCAAAATTTGAAGGATTCATGACACTGGGCA 2478
DB 2792 ATGGGAACATATCAATTTCTTGAGAAATCAAAATTTGAAGGATTCATGACACTGGGCA 2851
QY 2479 AATGAATTTAGCTCTTTACGTATAAAGAGCGGTTTATCTTAATATTAACGGCTCTTT 2538
DB 2852 AATGAATTTAGCTCTTTACGTATAAAGAGCGGTTTATCTTAATATTAACGGCTCTTT 2911
QY 2539 TTATAGAAAAATCCTTTAGCGTGGTTTTTTTCCGAAATGCTGGCGTACCCCAAGAAATTA 2598
DB 2912 TTATAGAAAAATCCTTTAGCGTGGTTTTTTTCCGAAATGCTGGCGTACCCCAAGAAATTA 2971
QY 2599 GAAATAGTATGATCAAAATTTTACGAAATAGATTCAGGAAATCAGATCCAACTAAAA 2658
DB 2972 GAAATAGTATGATCAAAATTTTACGAAATAGATTCAGGAAATCAGATCCAACTAAAA 3031
QY 2659 ACATAGCAAAATTTGCAAGTTTAACTAATCAACGCTAGTGTAGTTTAAATCCCAAT 2718
DB 3032 ACATAGCAAAATTTGCAAGTTTAACTAATCAACGCTAGTGTAGTTTAAATCCCAAT 3091
QY 2719 GAGCAACAGAACCCAGAGCCAGAAACAGAAATCAGAACAGTAACATTTGGAATTTAGAAATG 2778
DB 3092 GAGCAACAGAACCCAGAGCCAGAAACAGAAATCAGAACAGTAACATTTGGAATTTAGAAATG 3151
QY 2779 GAAGAGAAAAAGCAATGCTTGGTGTGAATTAATGCAAGAAATCGTTGCTTATTTTTT 2838
DB 3152 GAAGAGAAAAAGCAATGCTTGGTGTGAATTAATGCAAGAAATCGTTGCTTATTTTTT 3211

QY 2839 TTAAAAGCGGTATACCTAGATATACGAAACAAACGAACTGAATAGAAACGAAAAAGAGCC 2898
DB 3212 TTAAAAGCGGTATACCTAGATATACGAAACAAACGAACTGAATAGAAACGAAAAAGAGCC 3271
QY 2899 ATGACACATTTTATAAAATGTTTACGACATTTTAAATGATAGCCGATAGAAATTTGCC 2958
DB 3272 ATGACACATTTTATAAAATGTTTACGACATTTTAAATGATAGCCGATAGAAATTTGCC 3331
QY 2959 AAACCAACGCTTATCAGTTTACGATGAACTCTTCCCTCGTAAAGATTTTAAATTA 3018
DB 3332 AAACCAACGCTTATCAGTTTACGATGAACTCTTCCCTCGTAAAGATTTTAAATTA 3391
QY 3019 CTTTGTGTTGAAGACGGTATATAACCGTACTATCATATATAGGGAATCAGAGAGTTTC 3078
DB 3392 CTTTGTGTTGAAGACGGTATATAACCGTACTATCATATATAGGGAATCAGAGAGTTTC 3451
QY 3079 AAGTATCTAAGCTACTGAATTTAAGAAATTTAAGCAATCAATCGAAATCGTTTGAATG 3138
DB 3452 AAGTATCTAAGCTACTGAATTTAAGAAATTTAAGCAATCAATCGAAATCGTTTGAATG 3511
QY 3139 CTTTGTGTTTATCAATTTATAGAGGTGGATTTGTATGAATCATGATGAATTTAAACT 3198
DB 3512 CTTTGTGTTTATCAATTTATAGAGGTGGATTTGTATGAATCATGATGAATTTAAACT 3571
QY 3199 TATATAAAAAATAGTTTATGAGATAAAGAAATTTAGCAAAATATCTATACACTAGAAACG 3258
DB 3572 TATATAAAAAATAGTTTATGAGATAAAGAAATTTAGCAAAATATCTATACACTAGAAACG 3631
QY 3259 TTTTAAAGAGGTTTAAAGAAAGAAATATCTATTTAGAAACAAATTCAGATAAGTATTTT 3318
DB 3632 TTTTAAAGAGGTTTAAAGAAAGAAATATCTATTTAGAAACAAATTCAGATAAGTATTTT 3691
QY 3319 TCTTCGGAGGGGAGAGATTTATATATATTAAGTTTAAAGAAATTAACAAATTAATTTATTCG 3378
DB 3692 TCTTCGGAGGGGAGAGATTTATATATTAAGTTTAAAGAAATTAACAAATTAATTTATTCG 3751
QY 3379 ATTAGTGAAGAAAAATTTGACTTAAAGAAAAAAATCTTTTTTCAAAATCATGCAATATG 3438
DB 3752 ATTAGTGAAGAAAAATTTGACTTAAAGAAAAAAATCTTTTTTCAAAATCATGCAATATG 3811
QY 3439 AAACAGTTTGAATGAAGAAAGCAACCAAGTTAATTAACCAACCTATTTTATAGGATTTATA 3498
DB 3812 AAACAGTTTGAATGAAGAAAGCAACCAAGTTAATTAACCAACCTATTTTATAGGATTTATA 3871
QY 3499 GGAAGAGGAGAACAGCTGAATATCCCTTTTGTGTAGAAACTGTGCTTTCATGACGGC 3558
DB 3872 GGAAGAGGAGAACAGCTGAATATCCCTTTTGTGTAGAAACTGTGCTTTCATGACGGC 3931
QY 3559 TTGTTTAAAGTACAAATTTTAAAGTAAATTTGCTCAATCACTACCAAGCCAGTAAA 3618
DB 3932 TTGTTTAAAGTACAAATTTTAAAGTAAATTTGCTCAATCACTACCAAGCCAGTAAA 3991
QY 3619 AGCAAGGGGCTATTTTTCGCTATCGCTCAAAATCAAGCATGATTTGGCGTGGTGT 3678
DB 3992 AGCAAGGGGCTATTTTTCGCTATCGCTCAAAATCAAGCATGATTTGGCGTGGTGT 4051
QY 3679 GTTCTGACTTCCGAGGAGAGGATTTCAAGAAATCAAGATACATTTTACATTTGACACCC 3738
DB 4052 GTTCTGACTTCCGAGGAGAGGATTTCAAGAAATCAAGATACATTTTACATTTGACACCC 4111
QY 3739 AACGTTTATCGTTATGGAACGTTATGACAGCAACCGTTCATACAGAAAGGACATTTCT 3798
DB 4112 AACGTTTATCGTTATGGAACGTTATGACAGCAACCGTTCATACAGAAAGGACATTTCT 4171
QY 3799 GAAAAATTTTAAAGCAAAATCAATACCTTTCTTTATGATTTGATATTTACACCGGCAAAA 3858
DB 4172 GAAAAATTTTAAAGCAAAATCAATACCTTTCTTTATGATTTGATATTTACACCGGCAAAA 4231
QY 3859 GAACTATTTTACGCAAGGATTTTAAACCGCTATTTGATTTAGGTTTATGCTTACT 3918
DB 4232 GAACTATTTTACGCAAGGATTTTAAACCGCTATTTGATTTAGGTTTATGCTTACT 4291
QY 3919 ATGATTTTCAAAATCTGATAAAGGTTATCAAGCATATTTTGTGTTAGAAACCCAGTCTAT 3978

perfringens beta-toxin. Such a derivative is useful as a vaccine to induce an immune response and protect against Clostridium perfringens infection in man, pig, lamb, sheep, goat, calf and bird, which causes haemorrhagic enteritis, necrotic enteritis, enterotoxemia and lamb dysenteria. The new beta-toxin has been detoxified without impairing the immunogenicity, unlike prior art vaccines which used chemical and formalin detoxifying methods. Production of the beta-toxin in gram positive bacteria prevents prior art difficulties of isolation from dangerous Clostridium perfringens, and purification from the Clostridium perfringens spores

XX Sequence 5230 BP; 1930 A; 795 C; 983 G; 1522 T; 0 U; 0 Other;

Query Match 90.8%; Score 4993.4; DB 2; Length 5230;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4997; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 495 TCTAACTAGTACGCGTCTTAAACAAAGCCCGAAGGAGCTGAGTTGGCTGTGCCA 554
DB 228 TCTCTAGATGGATCCGGTCTTAAACAAAGCCCGAAGGAGCTGAGTTGGCTGTGCCA 287
QY 555 CCCTGAGCAATAACTAGCATACCCCTTGGGGCCCTTAAACGGGCTCTTGAAGGGTTTTT 614
DB 288 CCCTGAGCAATAACTAGCATACCCCTTGGGGCCCTTAAACGGGCTCTTGAAGGGTTTTT 347
QY 615 TCGTGAAGGAGCACTATATCCGGATGACCTGCGAGCAAGCTCTAGAAATCGATAGATT 674
DB 348 TCGTGAAGGAGCACTATATCCGGATGACCTGCGAGCAAGCTCTAGAAATCGATAGATT 407
QY 675 TTCAAGTGGCAACAGATAAATAAGCAGTTTAAATTTGTTGCTGAACCTTTTAAACCAAG 734
DB 408 TTGAAGTGGCAACAGATAAATAAGCAGTTTAAATTTGTTGCTGAACCTTTTAAACCAAG 467
QY 735 CAATACAACTATTGTGCGAACAGATAGCGACAGAGAGCGGAAACATTTGCTGTGCGA 794
DB 468 CAATACAACTATTGTGCGAACAGATAGCGACAGAGAGCGGAAACATTTGCTGTGCGA 527
QY 795 TCATTCATAAGCAATGCTTTCTTAAAGATAAAGCAATGATTAAGACATATCGATCAATA 854
DB 528 TCATTCATAAGCAATGCTTTCTTAAAGATAAAGCAATGATTAAGACATATCGATCAATA 587
QY 855 GTTTAGAAAAGATGTGATCCGTAGCGGTTTTTCAAAATTTTGAACAGCAATGATTTACT 914
DB 588 GTTTAGAAAAGATGTGATCCGTAGCGGTTTTTCAAAATTTTGAACAGCAATGATTTACT 647
QY 915 ATCCCTTTTATCAAGAGCGCAAAAGAAAACGAAATGATACCCCAATCAGTGCAGAAA 974
DB 648 ATCCCTTTTATCAAGAGCGCAAAAGAAAACGAAATGATACCCCAATCAGTGCAGAAA 707
QY 975 AGATATAATGGGAGATAAGACGGTTCGTGTTCTGCTGCTGCTGACCATATCATATAAAT 1034
DB 708 AGATATAATGGGAGATAAGACGGTTCGTGTTCTGCTGCTGCTGACCATATCATATAAAT 767
QY 1035 CGAAACAGCAAGAAATGGCGGAAACGTAAGAAAGTTATGGAATAAGACTTAGAAGCAA 1094
DB 768 CGAAACAGCAAGAAATGGCGGAAACGTAAGAAAGTTATGGAATAAGACTTAGAAGCAA 827
QY 1095 ACTTAAAGAGTGTGATAGTACGATCTTAAATTTTGTATATAGGAAATGAGTTA 1154
DB 828 ACTTAAAGAGTGTGATAGTACGATCTTAAATTTTGTATATAGGAAATGAGTTA 887
QY 1155 AATTAGATGCTAAAAATTTGTAAATTAAGAGGAGTGAATTACATGACAAAAATATAAAT 1214
DB 888 AATTAGATGCTAAAAATTTGTAAATTAAGAGGAGTGAATTACATGACAAAAATATAAAT 947
QY 1215 ATTCTCAAACTTTTAAACGGGTGAAGAGTACTCAACCAATTAATAAACCAATTTGAAT 1274
DB 948 ATTCTCAAACTTTTAAACGGGTGAAGAGTACTCAACCAATTAATAAACCAATTTGAAT 1007
QY 1275 TAAAAAGAAACCGATACCGTTTACGAAATTTGGAACAGGTAAGAGGCAATTTAAACGAGAAAC 1334
DB 1008 TAAAAAGAAACCGATACCGTTTACGAAATTTGGAACAGGTAAGAGGCAATTTAAACGAGAAAC 1067

1335 TGGCTAAATAAGTAAACAGGTAACGTCATTGAAATAGACAGATCATCTATTCAACTTAT 1394
DB 1068 TGGCTAAATAAGTAAACAGGTAACGTCATTGAAATAGACAGATCATCTATTCAACTTAT 1127
QY 1395 CGTCAGAAAAATTAACACTGAATCTGCTGTCACCTTTAAATTCACCAAGATATTCACAGT 1454
DB 1128 CGTCAGAAAAATTAACACTGAATCTGCTGTCACCTTTAAATTCACCAAGATATTCACAGT 1187
QY 1455 TTCAATTCCTTAAACAAACAGAGGTATAAATTTGTTGGAGTATTCCTTACCATTAAAGCA 1514
DB 1188 TTCAATTCCTTAAACAAACAGAGGTATAAATTTGTTGGAGTATTCCTTACCATTAAAGCA 1247
QY 1515 CACAAATTTAAATAAGTGTGTTTTGAAAGCCATGCGTCTGACATCTATCTGATTTGTT 1574
DB 1248 CACAAATTTAAATAAGTGTGTTTTGAAAGCCATGCGTCTGACATCTATCTGATTTGTT 1307
QY 1575 AAGAGAGTCTTCAAGCGTACCTTTGATATTTACCGCAACACTAGGTTGCTCTTGACA 1634
DB 1308 AAGAGAGTCTTCAAGCGTACCTTTGATATTTACCGCAACACTAGGTTGCTCTTGACA 1367
QY 1635 CTCAAGTCTCGAATTCAGCAATTTGCTTAAAGCTGCCAGCGGAATGCTTTCATCTTAAACCA 1694
DB 1368 CTCAAGTCTCGAATTCAGCAATTTGCTTAAAGCTGCCAGCGGAATGCTTTCATCTTAAACCA 1427
QY 1695 AAGTAAACAGTGTCTTAAATAAAGTACCGCCATACACAGATGTTCCAGATAAATATT 1754
DB 1428 AAGTAAACAGTGTCTTAAATAAAGTACCGCCATACACAGATGTTCCAGATAAATATT 1487
QY 1755 GGAAGCTATATACGCTACTTTGTTTCAAAATGGGCTCAATCGAGATATCGTCAACTGTTTA 1814
DB 1488 GGAAGCTATATACGCTACTTTGTTTCAAAATGGGCTCAATCGAGATATCGTCAACTGTTTA 1547
QY 1815 CTAAAAATCAGTTTCATCAAGCAATGAAACACGCGCAAGTAAACAAATTAAGTACCGTTTA 1874
DB 1548 CTAAAAATCAGTTTCATCAAGCAATGAAACACGCGCAAGTAAACAAATTAAGTACCGTTTA 1607
QY 1875 CTTATGAGCAAGTATTTGCTATTTTAAATAGTATCTATTATTAAACGGGAGGAAATAAT 1934
DB 1608 CTTATGAGCAAGTATTTGCTATTTTAAATAGTATCTATTATTAAACGGGAGGAAATAAT 1667
QY 1935 TCTATGAGTCCGCTTTTGTAAATTTGGAAGGTTACACGTTACTAAAGGGAATGTAGATAA 1994
DB 1668 TCTATGAGTCCGCTTTTGTAAATTTGGAAGGTTACACGTTACTAAAGGGAATGTAGATAA 1727
QY 1995 TTATTTAGTATACCTACTGACAGCTTCCAAAGAGCTTAAGAGGTCCTTAGCGCTCTTATCA 2054
DB 1728 TTATTTAGTATACCTACTGACAGCTTCCAAAGAGCTTAAGAGGTCCTTAGCGCTCTTATCA 1787
QY 2055 TGGGGAAGCTCGGATCATATGCAAGACAAATAAAGCTCGCAACAGCAGCTTTGGAGAAATGG 2114
DB 1788 TGGGGAAGCTCGGATCATATGCAAGACAAATAAAGCTCGCAACAGCAGCTTTGGAGAAATGG 1847
QY 2115 GACGAATCGAGAAAACCTCTTTTACGCTGGATTCATATCTAATAAGCCGTAAGGAGAC 2174
DB 1848 GACGAATCGAGAAAACCTCTTTTACGCTGGATTCATATCTAATAAGCCGTAAGGAGAC 1907
QY 2175 GGGTTCAAAAAGGTTTAAATAAGGAGAGCAATCAATGCAATAGCTAGTAACATATTTT 2234
DB 1908 GGGTTCAAAAAGGTTTAAATAAGGAGAGCAATCAATGCAATAGCTAGTAACATATTTT 1967
QY 2235 TTGACAAACGTTGGAGAAATTTAGAGAACGTCCTTCCAAAGCCAGTTTCAAGAGCTAGT 2294
DB 1968 TTGACAAACGTTGGAGAAATTTAGAGAACGTCCTTCCAAAGCCAGTTTCAAGAGCTAGT 2027
QY 2295 CACTTAAACATAAATTTAAACGCTATAAGTGTGGAACACTGTATATATATGAAAAAGCCG 2354
DB 2028 CACTTAAACATAAATTTAAACGCTATAAGTGTGGAACACTGTATATATATGAAAAAGCCG 2087
QY 2355 TAGAAGAAATTAAGAGCAAGAGGAGAAATTTAGAGAAATTTAATGCCATATGCGTGGCCGT 2414
DB 2088 TAGAAGAAATTAAGAGCAAGAGGAGAAATTTAGAGAAATTTAATGCCATATGCGTGGCCGT 2147
QY 2415 TAGATGGAGACATATCAATTTTCTTGAGAGATACAAATTTTGAAGGATTTACATGACACTG 2474

Db TAGAATGGGAACATATCAATTTCTTGGAGATACAAATTTGAAGGATTACATGACACTG 2207
Qy GCGAAATGAATTTACGTCCTTTACGTATAAAGAGCCGTTTATTTCTTTAATAATAACGGCT 2534
Db GCGAAATGAATTTACGTCCTTTACGTATAAAGAGCCGTTTATTTCTTTAATAATAACGGCT 2267
Qy CTTTATTTAGAAAATAATCTTTAGCGTGGTGTCTTTTTCGAAATGCTGCGGTACCCCAAGA 2594
Db CTTTATTTAGAAAATAATCTTTAGCGTGGTGTCTTTTTCGAAATGCTGCGGTACCCCAAGA 2327
Qy ATTAGAAATGATGATCAAAATTTATTCAGAAATGAGATCAGGAAATCAGATCCAAACAT 2654
Db ATTAGAAATGATGATCAAAATTTATTCAGAAATGAGATCAGGAAATCAGATCCAAACAT 2387
Qy AAAAACAATAGAAATAATGCAAGTTAACTAACTCAAGCTAGTAGTGGATTTAATCCC 2714
Db AAAAACAATAGAAATAATGCAAGTTAACTAACTCAAGCTAGTAGTGGATTTAATCCC 2447
Qy AAATGAGCCAAACAGAACCCAGAGCCAGAAACAGAAATCAGAAACAGTAACATTTGATTTAGA 2774
Db AAATGAGCCAAACAGAACCCAGAGCCAGAAACAGAAATCAGAAACAGTAACATTTGATTTAGA 2507
Qy AATGGAAGAAAGAAAGCAATGACTTCGTGTGGAATTAATGCAAGAAATCGTTGCTTATTT 2834
Db AATGGAAGAAAGAAAGCAATGACTTCGTGTGGAATTAATGCAAGAAATCGTTGCTTATTT 2567
Qy TTTTAAAGCCGTTATAGATATACGAAACCAAGCTGAATAGAAACGAAAGAAAG 2894
Db TTTTAAAGCCGTTATAGATATACGAAACCAAGCTGAATAGAAACGAAAGAAAG 2627
Qy AGCCATGACACATTTATAAATGTTGACGACATTTTATAAATGCATAGCCCGATAGAT 2954
Db AGCCATGACACATTTATAAATGTTGACGACATTTTATAAATGCATAGCCCGATAGAT 2687
Qy TGCCAAACCAAGCTTATCAGTTAGTACAGATGAATCTTCCCTCGTGAAGATTTATTTAA 3014
Db TGCCAAACCAAGCTTATCAGTTAGTACAGATGAATCTTCCCTCGTGAAGATTTATTTAA 2747
Qy TTAACCTTTGTTTGAAGCCGTTATATAACCGTACTATCATTTATATAGGAAATCAGAGAGT 3074
Db TTAACCTTTGTTTGAAGCCGTTATATAACCGTACTATCATTTATATAGGAAATCAGAGAGT 2807
Qy TTTCAAGTATCTAAGCTACTGAAATTTAAGAAATGTTAAGCAATCAATCGGAAATCGTTTG 3134
Db TTTCAAGTATCTAAGCTACTGAAATTTAAGAAATGTTAAGCAATCAATCGGAAATCGTTTG 2867
Qy ATTGCTTTTGTATTTATTTATAGAAAGTGGAGTTTGTATGAATCATGATGAATGTAA 3194
Db ATTGCTTTTGTATTTATTTATAGAAAGTGGAGTTTGTATGAATCATGATGAATGTAA 2927
Qy AACTATATAAATAATGATTTATGGAAGATGAAGAAATAGCAATATCTATACACTAGA 3254
Db AACTATATAAATAATGATTTATGGAAGATGAAGAAATAGCAATATCTATACACTAGA 2987
Qy AACGTTTAAAGAAAGATTTAGAAAGAGAAATATCTACTTGAACAAATAACAGATAAGTA 3314
Db AACGTTTAAAGAAAGATTTAGAAAGAGAAATATCTACTTGAACAAATAACAGATAAGTA 3047
Qy TTTTCTTCGAGGGGGAGATTTATATATATAGTTAATAGAAATAACAAATAATTTA 3374
Db TTTTCTTCGAGGGGGAGATTTATATATATAGTTAATAGAAATAACAAATAATTTA 3107
Qy TTCGATTAGTGAAGAAATTTGACTTTAAGAGGAAATAATCTTTTTCGAAACATGCAAT 3434
Db TTCGATTAGTGAAGAAATTTGACTTTAAGAGGAAATAATCTTTTTCGAAACATGCAAT 3167
Qy ATTGAAACAGTTGATGAAAGCAACCAAGTTTAAATTAACAAACCTTATTTTAGGATT 3494
Db ATTGAAACAGTTGATGAAAGCAACCAAGTTTAAATTAACAAACCTTATTTTAGGATT 3227
Qy TATAGGAAGGAGACAGCTGAATGAATATCCCTTTGTTGTAAGAACTGCTTCATGA 3554

Db TATAGGAAGGAGACAGCTGAATGAATATCCCTTTTGTGTAGAAACTGTGCTTCATGA 3287
Qy CCGCTTGTAAAGTACAAATTTTAAATAATAGTAAATTCGCTCAATCACTACCAAGCCAGG 3614
Db CCGCTTGTAAAGTACAAATTTTAAATAATAGTAAATTCGCTCAATCACTACCAAGCCAGG 3347
Qy TAAAGCAAAAGGGGCTATTTTTCGCTATCGCTCAAAATCAAGCATGATGCGGTGCGTGG 3674
Db TAAAGCAAAAGGGGCTATTTTTCGCTATCGCTCAAAATCAAGCATGATGCGGTGCGTGG 3407
Qy TGTGTTCTGACTTCGAGGAGCGGATTTCAAGAAATCAAGATACATTTACACATTCGAC 3734
Db TGTGTTCTGACTTCGAGGAGCGGATTTCAAGAAATCAAGATACATTTACACATTCGAC 3467
Qy ACCCAACGTTTATCGTTATGGAACGTTATGCAAGCAAAACCGTTTCATACGAAAGGACA 3794
Db ACCCAACGTTTATCGTTATGGAACGTTATGCAAGCAAAACCGTTTCATACGAAAGGACA 3527
Qy TTCTGAAACCAATTTAAGACAAATCAATACCTTCTTTATGATTTGATTTACACGGC 3854
Db TTCTGAAACCAATTTAAGACAAATCAATACCTTCTTTATGATTTGATTTACACGGC 3587
Qy ABAAGAACTATTTTCAGCAAGCGATTTTAAACACCGCTATGATTTAGGTTTATGCC 3914
Db ABAAGAACTATTTTCAGCAAGCGATTTTAAACACCGCTATGATTTAGGTTTATGCC 3647
Qy TACTATGATTTCAAAATCTGATAAGGTTATCAAGCATATTTGTTTGAAGAACGCCAGT 3974
Db TACTATGATTTCAAAATCTGATAAGGTTATCAAGCATATTTGTTTGAAGAACGCCAGT 3707
Qy CTATGCTACTTCAAAATCAGAAATTTAATCTGTAAGCAAGCAATTTGTTTGAAGAACGCCAGT 4034
Db CTATGCTACTTCAAAATCAGAAATTTAATCTGTAAGCAAGCAATTTGTTTGAAGAACGCCAGT 3767
Qy TATCCGAGAAATTTTGGAAAGTCTTTGCCAGTTGATCTAACGTTAATCATTTTGGTAT 4094
Db TATCCGAGAAATTTTGGAAAGTCTTTGCCAGTTGATCTAACGTTAATCATTTTGGTAT 3827
Qy TGCTCGCATACAGAACCGCAATGTAGAAATTTTTCGATCCTAATTTACCGTTATCTTT 4154
Db TGCTCGCATACAGAACCGCAATGTAGAAATTTTTCGATCCTAATTTACCGTTATCTTT 3887
Qy CAAAGAAATGGCAAGATTTGCTTTTCAAAACAAACAGATAATAGGGCTTTACTCGTTCAAG 4214
Db CAAAGAAATGGCAAGATTTGCTTTTCAAAACAAACAGATAATAGGGCTTTACTCGTTCAAG 3947
Qy TCTAACCGTTTAAAGCGGTACAGAGGCAAAACCAAGTAGATGAACCTCGTTAATCT 4274
Db TCTAACCGTTTAAAGCGGTACAGAGGCAAAACCAAGTAGATGAACCTCGTTAATCT 4007
Qy CTTATTGCAAGAAAGCAAAATTTTTCAGGAGAAAGGGTTTATAGGGCGTATACGTCAT 4334
Db CTTATTGCAAGAAAGCAAAATTTTTCAGGAGAAAGGGTTTATAGGGCGTATACGTCAT 4067
Qy GTTTACCCCTCTCTTTAGCCTACTTTAGTTTACGCTTATTTCAATTCGAAACGTCGGAATAA 4394
Db GTTTACCCCTCTCTTTAGCCTACTTTAGTTTACGCTTATTTCAATTCGAAACGTCGGAATAA 4127
Qy TATGTTTGAATTTAATATCGATTTAGATCAACCTTTGAAGAAAGAAAGTAATCAAAAT 4454
Db TATGTTTGAATTTAATATCGATTTAGATCAACCTTTGAAGAAAGAAAGTAATCAAAAT 4187
Qy TGTAGAAAGTGCCTATTTCAGAAACCTATCAAGGGGCTAATAGGGAATACATTAACATCT 4514
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Qy TTGCAAAAGCTTGGGTATCAAGTGAATTTAACAGTAAGATTTTATTTGCTCCGTCAGGGTG 4574
Db TTGCAAAAGCTTGGGTATCAAGTGAATTTAACAGTAAGATTTTATTTGCTCCGTCAGGGTG 4307
Qy GTTTAAATTCAGAAAGAAAGGAGCAAGCTGTTTCAAGCTGTTTATTTGTCAGAAATGGAAGA 4634
Db GTTTAAATTCAGAAAGAAAGGAGCAAGCTGTTTCAAGCTGTTTATTTGTCAGAAATGGAAGA 4367

QY 4635 AGATTTAATGCTTATATTAGCGAAGGAGTATATCAAGCCCTATTATTAGTACGAC 4694
Db 4368 AGATTTAATGCTTATATTAGCGAAGGAGTATATCAAGCCCTATTATTAGTACGAC 4427
QY 4695 CAAAAAGAGATTAGAGAGTGTAGGCAATCTCTGAACGACATTTAGATAAATTTGCTGAA 4754
Db 4428 CAAAAAGAGATTAGAGAGTGTAGGCAATCTCTGAACGACATTTAGATAAATTTGCTGAA 4487
QY 4755 GGTACTGAAGCGAATCAGAGAAATTTCTTTAGATTAAACCGAGGAGAAATGCTGGCAT 4814
Db 4488 GGTACTGAAGCGAATCAGAGAAATTTCTTTAGATTAAACCGAGGAGAAATGCTGGCAT 4547
QY 4815 TCAACTTGCTAGTGTAAATCAATTTGCTGATCGATCAATTTAAAGTAAAGGAGGAGAA 4874
Db 4548 TCAACTTGCTAGTGTAAATCAATTTGCTGATCGATCAATTTAAAGTAAAGGAGGAGAA 4607
QY 4875 AGAAAGCTATATAAGCGCTGACAAATTTCTTTGACTTAGAGATACATTTCAATCAAGA 4934
Db 4608 AGAAAGCTATATAAGCGCTGACAAATTTCTTTGACTTAGAGATACATTTCAATCAAGA 4667
QY 4935 GACTTTAAACAGCTAGCAGACGCTTAAACCGGACACACACTCGATTTGTTAGCTA 4994
Db 4668 GACTTTAAACAGCTAGCAGACGCTTAAACCGGACACACACTCGATTTGTTAGCTA 4727
QY 4995 TGATACAGGCTGAAATPAAACCCGCACTATGCCATTTACATTTATATCTATGATAGCTGT 5054
Db 4728 TGATACAGGCTGAAATPAAACCCGCACTATGCCATTTACATTTATATCTATGATAGCTGT 4787
QY 5055 TTGTTTTTCTTCTGCTTTTAGCGAATGATTAGCAGAAATATACAGATGAGATTTTAAAT 5114
Db 4788 TTGTTTTTCTTCTGCTTTTAGCGAATGATTAGCAGAAATATACAGATGAGATTTTAAAT 4847
QY 5115 TAATTTATAGGGGAGAGAGAGTAGCCCGAAACCTTTTAGTTGGCTTGGACTGAAC 5174
Db 4848 TAATTTATAGGGGAGAGAGAGTAGCCCGAAACCTTTTAGTTGGCTTGGACTGAAC 4907
QY 5175 GAAGTGAAGGAGAGCTAAACGTCGAGGGGCGATGAGACGAGGAGGAACTTGAT 5234
Db 4908 GAAGTGAAGGAGAGCTAAACGTCGAGGGGCGATGAGACGAGGAGGAACTTGAT 4967
QY 5235 TTTTAAATTTCTATCTTTTATAGTTCATTAGATGATATCTTTTCTCTATAAATTT 5294
Db 4968 TTTTAAATTTCTATCTTTTATAGTTCATTAGATGATATCTTTTCTCTATAAATTT 5027
QY 5295 TAGCAGCAATATAGATTTATGATAGGTCATTTAAAGTTGAGCATATTAGAGGAGGAAA 5354
Db 5028 TAGCAGCAATATAGATTTATGATAGGTCATTTAAAGTTGAGCATATTAGAGGAGGAAA 5087
QY 5355 TCTTGAGGAATATTTGAAGACCCGATTCATGATGATGATGATTTCTTGTTAGTAT 5414
Db 5088 TCTTGAGGAATATTTGAAGACCCGATTCATGATGATGATGATTTCTTGTTAGTAT 5147
QY 5415 GGTTTTAACTAAAGTAGTGAATTTTGTATTTTGTGTTGTTGTTGTTGTTGTTGTTGTT 5474
Db 5148 GGTTTTAACTAAAGTAGTGAATTTTGTATTTTGTGTTGTTGTTGTTGTTGTTGTTGTT 5207
QY 5475 TTGCTAGTCAAGTGATTAATA 5497
Db 5208 TTGCTAGTCAAGTGATTAATA 5230

RESULT 6

AAAL5041

AC AAAL5041 standard; DNA; 5230 BP.

XX AAAL5041;

XX AAAL5041;

DT 21-AUG-2000 (first entry)

XX Nucleotide sequence of expression plasmid pTRX1.

DE Intestinal mucosa; cytokine; cytokine antagonist; anti-inflammatory;

XX Intestinal mucosa; cytokine; cytokine antagonist; anti-inflammatory;

KW Gran-positive bacteria; Lactococcus lactis; gastrointestinal tract;
KW inflammatory bowel disease; chronic colitis; Crohn's disease; IL10;
KW ulcerative colitis; tumour necrosis factor; TNF; interleukin 10; ss.
OS Synthetic.
XX WO200023471-A2.
XX 27-APR-2000.
XX 06-OCT-1999; 99WO-EP007800.
XX 20-OCT-1998; 98EP-00203529.
XX (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX Steidler L, Remaut ER, Fiers W;
XX WPI; 2000-422481/36.
XX Treating inflammatory bowel diseases comprises administering a
composition comprising a cytokine-producing or cytokine antagonist-
producing Gram-positive bacterial strain.
XX Disclosure; Fig 1B; 45pp; English.
XX The present sequence represents an expression plasmid for use in the
course of the invention. The specification describes an administration
strategy for the delivery of the intestinal mucosa of cytokines or
cytokine antagonists, preferably of acid sensitive anti-inflammatory
agents such as interleukin 10 (IL10) or tumour necrosis factor (TNF). The
method uses a cytokine-producing or cytokine antagonist-producing Gram-
positive bacterial strain (such as Lactococcus lactis). The use of non-
colonizing bacteria expressing cytokines or cytokine antagonists allows
the treatment to be directed to the disease site, whilst minimizing the
possibility of degradation along the gastrointestinal tract. The
recombinant bacteria are used in the treatment of inflammatory bowel
diseases, especially chronic colitis, Crohn's disease or an ulcerative
colitis
SQ Sequence 5230 BP; 1930 A; 796 C; 982 G; 1522 T; 0 U; 0 Other;

Query Match 90.8%; Score 4991.8; DB 3; Length 5230;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4996; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 495 TCTAACTAGTAGTCCGCTGCTAACAAAGCCGAAAGAGAGCTGAGTTGGCTGCTGCCA 554
Db 228 TCTCTAGATGATCGGCTGCTAACAAAGCCGAAAGAGAGCTGAGTTGGCTGCTGCCA 287
QY 555 CGCTGACCAATACTAGCATACCCCTTGGGGCTCTAAACGGGCTCTTGAGGGGTTTTT 614
Db 288 CGCTGACCAATACTAGCATACCCCTTGGGGCTCTAAACGGGCTCTTGAGGGGTTTTT 347
QY 615 TGCTGAAAGGAGGAACTATATCCGATGACCTGAGCAAGCTCTAGAAATCGATACGATT 674
Db 348 TGCTGAAAGGAGGAACTATATCCGATGACCTGAGCAAGCTCTAGAAATCGATACGATT 407
QY 675 TTGAAGTGGCAACAGATAAAAAAGCAGTTTAAATTTGTTGCTGAACTTTTAAACAAAG 734
Db 408 TTGAAGTGGCAACAGATAAAAAAGCAGTTTAAATTTGTTGCTGAACTTTTAAACAAAG 467
QY 735 CAATACATCATTTGCTCCACAGATAGCGACAGAGAGGCGAAACATTCCTCGTCCGA 794
Db 468 CAATACATCATTTGCTCCACAGATAGCGACAGAGAGGCGAAACATTCCTCGTCCGA 527
QY 795 TCATTATAAAGCAATGCTTTTCTTAAAGATAAAACGTATAAAAGACTATGGATCAATA 854
Db 528 TCATTATAAAGCAATGCTTTTCTTAAAGATAAAACGTATAAAAGACTATGGATCAATA 587
QY 855 GTTTAGAAAAGATGATCGTAGCGGTTTTTCAAAATTTGCAACCCAGGATGATTAAT 914
Db 588 GTTTAGAAAAGATGATCGTAGCGGTTTTTCAAAATTTGCAACCCAGGATGATTAAT 647

Db 2808 TTTCAAGATCTAAGCTACTGAATTTAAGAAATGTTAAGCAATCAATCGGAATCGTTG 2867
Qy 3135 ATTGCTTTTGTGATTCATTTATAGAAAGTGAGTTGTATGAATCATGATGAATGTAA 3194
Db 2868 ATTGCTTTTGTGATTCATTTATAGAAAGTGAGTTGTATGAATCATGATGAATGTAA 2927
Qy 3195 AACTTATATAAAATAGTTTATTGGAGATAAGAAATTAGCAATATCTATACACTAGA 3254
Db 2928 AACTTATATAAAATAGTTTATTGGAGATAAGAAATTAGCAATATCTATACACTAGA 2987
Qy 3255 AACTTTTAAAGAGATTAGAAAGAGAAATATCTACTTAGAAACAAAATCAGATAAGTA 3314
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Qy 3315 TTTTCTTCGAGGGGAGATATATATATAGTTTAATAGAAATAACAAATATATTTA 3374
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Qy 3375 TTCGATTAGTGGAAAAATAGCTTATAAAGGAAAAATCTTTTCAAAACATGCAAT 3434
Db 3108 TTCGATTAGTGGAAAAATAGCTTATAAAGGAAAAATCTTTTCAAAACATGCAAT 3167
Qy 3435 ATTGAACAGTTGATGAAAGAGCAACCAAGTTAATTAACCACTATTTTATAGATT 3494
Db 3168 ATTGAACAGTTGATGAAAGAGCAACCAAGTTAATTAACCACTATTTTATAGATT 3227
Qy 3495 TATAGGAAAGAGCAACAGCTGAATGAATATCCCTTTTGTGTAGAACTGTGCTCATGA 3554
Db 3228 TATAGGAAAGAGCAACAGCTGAATGAATATCCCTTTTGTGTAGAACTGTGCTCATGA 3287
Qy 3555 CGGCTTGTTAAAGTACAAATTTAAATATAGTAAATTCGCTCAATCACTACCAAGCCAGG 3614
Db 3288 CGGCTTGTTAAAGTACAAATTTAAATATAGTAAATTCGCTCAATCACTACCAAGCCAGG 3347
Qy 3615 TAAAGCAAAAGGGGCTATTTTGGGTATCGCTCAAAATCAAGCATGATTCGGCGTCTGG 3674
Db 3348 TAAAGCAAAAGGGGCTATTTTGGGTATCGCTCAAAATCAAGCATGATTCGGCGTCTGG 3407
Qy 3675 TGTGTTCTGACTCCGAGGAAGCGATTCAAGAAATCAAGATACATTTACATTTGGAC 3734
Db 3408 TGTGTTCTGACTCCGAGGAAGCGATTCAAGAAATCAAGATACATTTACATTTGGAC 3467
Qy 3735 ACCCAAGTTTATCGTTATCGNAGCTATGAGCGAAACCGTTTCATACAGAAAGACA 3794
Db 3468 ACCCAAGTTTATCGTTATGGAAGCTATGAGCGAAACCGTTTCATACAGAAAGACA 3527
Qy 3795 TTCTGAAAAACAAATTAAGACAAATCAATACCTTCTTTTATTTGATTTTCAACCGC 3854
Db 3528 TTCTGAAAAACAAATTAAGACAAATCAATACCTTCTTTTATTTGATTTTCAACCGC 3587
Qy 3855 AAAAGAACTATTTACGACAGCGATTTTAAACACCGCTATTTGATTTAGGTTTATGCC 3914
Db 3588 AAAAGAACTATTTACGACAGCGATTTTAAACACCGCTATTTGATTTAGGTTTATGCC 3647
Qy 3915 TACTATGATTATCAAAATCTGATAAGGTATCAAGCATATTTTGTTTTAAAGACGCCAGT 3974
Db 3648 TACTATGATTATCAAAATCTGATAAGGTATCAAGCATATTTTGTTTTAAAGACGCCAGT 3707
Qy 3975 CTATGTCATCAAAATCAGAAATTTAAATCTGTCAAAAGCAGCCAAAATATTTTCGAAAA 4034
Db 3708 CTATGTCATCAAAATCAGAAATTTAAATCTGTCAAAAGCAGCCAAAATATTTTCGAAAA 3767
Qy 4035 TATCGGAGATATTTTCGAAAGCTTTTCCAGTTTGTATCAACGTGTAATCATTTTGTAT 4094
Db 3768 TATCGGAGATATTTTGAAGAGCTTTTCCAGTTTGTATCAACGTGTAATCATTTTGTAT 3827
Qy 4095 TGCTCGCATACCAAGAACGGAATGTAGAAATTTTGTATCTTAATACCGTTATTTCTTT 4154
Db 3828 TGCTCGCATACCAAGAACGGAATGTAGAAATTTTGTATCTTAATACCGTTATTTCTTT 3887
Qy 4155 CAAGATGGAAGATTTGCTTTTCAACAAACAGATAAAGGGCTTTACTGTTCAAG 4214

Db 3888 CAAAGATGCGCAAGATTGGTCTTTTCAAAACAAACAGATAAAGGGCTTTTACTCGTTCAAG 3947
Qy 4215 TCTAACGGTTTTTAAGCGGTACAGAGGCAAAACAAAGTAGATGAACCTCGTTTAAATCT 4274
Db 3948 TCTAACGGTTTTTAAGCGGTACAGAGGCAAAACAAAGTAGATGAACCTCGTTTAAATCT 4007
Qy 4275 CTTATTGCAACGAAACGAAATTTTTCAGGAGAAAAAGGGTTTAAATAGGCGTAATAACGTCAT 4334
Db 4008 CTTATTGCAACGAAACGAAATTTTTCAGGAGAAAAAGGGTTTAAATAGGCGTAATAACGTCAT 4067
Qy 4335 GTTTACCTCTCTTTAGGCTACTTTTAGTTCAAGGCTATTTCAATCGAAACGTCGGATATAA 4394
Db 4068 GTTTACCTCTCTTTAGGCTACTTTTAGTTCAAGGCTATTTCAATCGAAACGTCGGATATAA 4127
Qy 4395 TATGTTTCAGTTTAAATATCGATTAGATCAACCCCTTAGAAGAAAAAGAAATTAATCAAAAT 4454
Db 4128 TATGTTTCAGTTTAAATATCGATTAGATCAACCCCTTAGAAGAAAAAGAAATTAATCAAAAT 4187
Qy 4455 TGTTAGAGTGCCTTATCAGAAAACTATCAAGGGCTAATAGGAGTAATACATTTCT 4514
Db 4188 TGTTAGAGTGCCTTATCAGAAAACTATCAAGGGCTAATAGGAGTAATACATTTCT 4247
Qy 4515 TTGCAAGCTTGGGTATCAAGTGATTTAAACAGTAAGATTTATTTGTCGGTCAAGGGTG 4574
Db 4248 TTGCAAGCTTGGGTATCAAGTGATTTAAACAGTAAGATTTATTTGTCGGTCAAGGGTG 4307
Qy 4575 GTTTAAATTCAGAAAAAAGAGCGCAACGTCCTCAACGCTTCTCATTTGTCAGAAATGAAAGA 4634
Db 4308 GTTTAAATTCAGAAAAAAGAGCGCAACGTCCTCAACGCTTCTCATTTGTCAGAAATGAAAGA 4367
Qy 4635 AGATTTAATGCTTATATTTAGCGAAAAAAGCGATGTATACAGCCCTTATTTAGTCAACGAC 4694
Db 4368 AGATTTAATGCTTATATTTAGCGAAAAAAGCGATGTATACAGCCCTTATTTAGTCAACGAC 4427
Qy 4695 CAAAAAGAGATTAGAGAAAGTGTAGGCAATTCCTGAACGACATTTAGATAAATTTCTCTGAA 4754
Db 4428 CAAAAAGAGATTAGAGAAAGTGTAGGCAATTCCTGAACGACATTTAGATAAATTTCTCTGAA 4487
Qy 4755 GGTACTGAAGCGCAATCAGAAATTTTCTTTAAGATTTAAACAGGAAAGATTTGTTGGCAT 4814
Db 4488 GGTACTGAAGCGCAATCAGAAATTTTCTTTAAGATTTAAACAGGAAAGATTTGTTGGCAT 4547
Qy 4815 TCACCTTGCTAGTGTAAATCATTTGCTATCGATCATTTAAAGTAAAAAAGAAAGAAAA 4874
Db 4548 TCACCTTGCTAGTGTAAATCATTTGCTATCGATCATTTAAGTAAAAAAGAAAGAAAA 4607
Qy 4875 AGAAAGCTATATAAAGCGCTGACAAATCTTTTGAATTTAGAGCATACATTTCAAGA 4934
Db 4608 AGAAAGCTATATAAAGCGCTGACAAATCTTTTGAATTTAGAGCATACATTTCAAGA 4667
Qy 4935 GACTTTAAACAGCTAGCAGACGCGCTTAAACGAGACACAACTCGATTTGTTTAGCTA 4994
Db 4668 GACTTTAAACAGCTAGCAGACGCGCTTAAACGAGACACAACTCGATTTGTTTAGCTA 4727
Qy 4995 TGATACAGCTGAAAAATAAACCCGCACTATGCCATTTACATTTATATCTATGATCGTGT 5054
Db 4728 TGATACAGCTGAAAAATAAACCCGCACTATGCCATTTACATTTATCTATGATCGTGT 4787
Qy 5055 TTGTTTTTTTCTTTGCTTTTAGCGAATGATTAGCGAAATATACAGAGTAAGATTTAAT 5114
Db 4788 TTCTTTTCTTTGCTTTTAGCGAATGATTAGCGAATATACAGAGTAAGATTTAAT 4847
Qy 5115 TAATTATTAGGCGGAGAGAGAGAGTAGCCCGAAAACTTTTAGTTGGCTTGGACTGAAC 5174
Db 4848 TAATTATTAGGCGGAGAGAGAGTAGCCCGAAAACTTTTAGTTGGCTTGGACTGAAC 4907
Qy 5175 GAAGTGAAGGAGGCTACTAAAAAGTCAAGGGGAGTGAGAGCGAAGCGAAGCACTTGAT 5234
Db 4908 GAAGTGAAGGAGGCTACTAAAAAGTCAAGGGGAGTGAGAGCGAAGCGAAGCACTTGAT 4967
Qy 5235 TTTTAAATTTTCTATCTTTTATAGTCAATAGAGTATCTTTATTTGCTCTATAAACTATT 5294
Db 4968 TTTTAAATTTTCTATCTTTTATAGTCAATAGAGTATCTTTATTTGCTCTATAAACTATT 5027

QY	5295	TAGCAGCATATATAGATTATTGAAATAGGTCATTTAAAGTTGAGCATATTAGAGGAGGAAAA	5354
Db	5028	TAGCAGCATATATAGATTATTGAAATAGGTCATTTAAAGTTGAGCATATTAGAGGAGGAAAA	5087
QY	5355	TCTTGGAGAAATATTGAAGAACCCGATTACATGATTGGATTAGTTCTTGTGTTACGT	5414
Db	5088	TCTTGGAGAAATATTGAAGAACCCGATTACATGATTGGATTAGTTCTTGTGTTACGT	5147
QY	5415	GGTTTTTAACATAAAGTAGTGAATTTTGAATTTTGGTGTGTGTCTTGTGTTAGTAT	5474
Db	5148	GGTTTTTAACATAAAGTAGTGAATTTTGAATTTTGGTGTGTGTCTTGTGTTAGTAT	5207
QY	5475	TTGCTAGTCAAGTGATTAATA	5497
Db	5208	TTGCTAGTCAAGTGATTAATA	5230
RESULT 7			
AA07548			
ID	AA07548 standard; DNA; 5216 BP.		
XX			
AC	AA07548;		
XX			
DT	08-JUN-1999 (first entry)		
XX			
DE	pKS90 TIR coupling vector.		
XX			
KW	Beta-toxin; cpb; vaccine; infection; protection; retained immunogenicity;		
KW	haemorrhagic enteritis; necrotic enteritis; enterotoxemia;		
KW	lamb dysentery; translation initiation region; ds.		
XX			
OS	Synthetic.		
XX			
PN	EP892054-AL.		
XX			
PD	20-JAN-1999.		
XX			
PF	17-JUN-1998; 98EP-00202032.		
XX			
PR	20-JUN-1997; 97EP-00201888.		
XX			
PA	(ALXU) AKZO NOBEL NV.		
XX			
PI	Sergers RPAM, Waterfield NR, Frandsen PL, Wells JW;		
XX			
DR	WPI; 1999-083571/08.		
XX			
PT	New detoxified derivative of Clostridium perfringens beta-toxin - with		
PT	retained immunogenicity, useful as a vaccine to protect against		
PT	Clostridium perfringens infection.		
XX			
PS	Example; Fig 2b; 30pp; English.		
XX			
CC	The sequence is that of the vector pKS90 which was used in the		
CC	construction of a detoxified immunogenic derivative of Clostridium		
CC	perfringens beta-toxin. Such a derivative is useful as a vaccine to		
CC	induce an immune response and protect against Clostridium perfringens		
CC	infection in man, pig, lamb, sheep, goat, calf and bird, which causes		
CC	haemorrhagic enteritis, necrotic enteritis, enterotoxemia and lamb		
CC	dysentery. The new beta-toxin has been detoxified without impairing the		
CC	immunogenicity, unlike prior art vaccines which used chemical and		
CC	formalin detoxifying methods. Production of the beta-toxin in gram		
CC	positive bacteria prevents prior art difficulties of isolation from		
CC	dangerous Clostridium perfringens, and purification from the Clostridium		
CC	perfringens spores		
XX			
SQ	Sequence 5216 BP; 1934 A; 790 C; 980 G; 1512 T; 0 U; 0 Other;		
Query Match 90.6%; Score 4982.4; DB 2; Length 5216;			
Best Local Similarity 99.9%; Pred. No. 0;			
Matches 4997; Conservative 0; Mismatches 6; Indels 1; Gaps 1;			

QY	494	TTCTAACTAGTAGTCCGGCTCTTAAAGAGCCGAAAGAGAGAGTGTGGCTGCTGCC	553
DB	214	TCCAAATGATCAGATCCGGCTCTTAAAGAGCCGAAAGAGAGTGTGGCTGCTGCC	273
QY	554	ACCGCTGAGCAATACTAGTAAACCCCTTGGGGCTCTTAAACGGGTCTTGGGGGTTTT	613
DB	274	ACCGCTGAGCAATACTAGTAAACCCCTTGGGGCTCTTAAACGGGTCTTGGGGGTTTT	333
QY	614	TTGCTGAAAGGAGGAACTATATCCGGATGACCTCGAGGCAAGCTCTAGAAATCGATAC	673
DB	334	TTGCTGAAAGGAGGAACTATATCCGGATGACCTCGAGGCAAGCTCTAGAAATCGATAC	393
QY	674	TTTGAAGTGGCAACAGATAAAGGAGGAGTAAATTTGCTGAACTTTTAAACAA	733
DB	394	TTTGAAGTGGCAACAGATAAAGGAGGAGTAAATTTGCTGAACTTTTAAACAA	453
QY	734	GCAAAATACAATCATTTGTCGCAACAGATAGCGACAGAGAGGCGAAACATTTGCTGTCG	793
DB	454	GCAAAATACAATCATTTGTCGCAACAGATAGCGACAGAGAGGCGAAACATTTGCTGTCG	513
QY	794	ATCATTATAAAGCAAAATCCCTTTTCTTAAAGTAAACGTAATAAAGACTATGATCAAT	853
DB	514	ATCATTATAAAGCAAAATCCCTTTTCTTAAAGTAAACGTAATAAAGACTATGATCAAT	573
QY	854	AGTTTAGAAAAGATGTGATCCGTAGCGGTTTCAAAATTTGCAACACAGGATGATTTAC	913
DB	574	AGTTTAGAAAAGATGTGATCCGTAGCGGTTTCAAAATTTGCAACACAGGATGATTTAC	633
QY	914	TATCCCTTTTATCAAGAGCGCAAAAGAAACGAAATGATACCAATCAGTGCAGAAA	973
DB	634	TATCCCTTTTATCAAGAGCGCAAAAGAAACGAAATGATACCAATCAGTGCAGAAA	693
QY	974	AAAGTATATGGAGATAGAGCGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1033
DB	694	AAAGTATATGGAGATAGAGCGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	753
QY	1034	TCGAAACAGCAAAAGAAATGCGGAAACGTAAGAAAGAGTTATGAAATAGACTTAAAGCA	1093
DB	754	TCGAAACAGCAAAAGAAATGCGGAAACGTAAGAAAGAGTTATGAAATAGACTTAAAGCA	813
QY	1094	AACTTAAGAGTGTGTGATAGTGCAGTATCTTAAATTTGCTATATAGGATTTGAGCTT	1153
DB	814	AACTTAAGAGTGTGTGATAGTGCAGTATCTTAAATTTGCTATATAGGATTTGAGCTT	873
QY	1154	AAATTAGATGCTAAAAATTTGTAATTTAAGAGAGGAGTATCATGAAACAAATAATAAAA	1213
DB	874	AAATTAGATGCTAAAAATTTGTAATTTAAGAGAGGAGTATCATGAAACAAATAATAAAA	933
QY	1214	TATCTCAAACTTTTAAAGAGTAAAGAGTCTCAACCAATTAATAAACAATTTGAT	1273
DB	934	TATCTCAAACTTTTAAAGAGTAAAGAGTCTCAACCAATTAATAAACAATTTGAT	993
QY	1274	TTAAAGAAACCGATACCGTTTACGAAATTTGAAACAGAGTAAAGGCGATTTAACGACGAA	1333
DB	994	TTAAAGAAACCGATACCGTTTACGAAATTTGAAACAGAGTAAAGGCGATTTAACGACGAA	1052
QY	1334	CTGGCTTAAATTAAGTAAACAGGTAACGTTTATTTGAATTTAGACAGTCTATTTCAACTTA	1393
DB	1053	CTGGCTTAAATTAAGTAAACAGGTAACGTTTATTTGAATTTAGACAGTCTATTTCAACTTA	1112
QY	1394	TCGTGAGAAAATTTAAATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1453
DB	1113	TCGTGAGAAAATTTAAATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1172
QY	1454	TTTCAATTTCCCTTAAACAGAGGATATAAAATTTGTTGGAGTATTTCTTACATTTAAGC	1513
DB	1173	TTTCAATTTCCCTTAAACAGAGGATATAAAATTTGTTGGAGTATTTCTTACATTTAAGC	1232
QY	1514	ACACAAATTTTAAAGAGTGTGTTTGAAGCCATCGCTGACATCTATCTGATCTT	1573
DB	1233	ACACAAATTTTAAAGAGTGTGTTTGAAGCCATCGCTGACATCTATCTGATCTT	1292
QY	1574	GAAGAAGGATTTCTACAAGCGTACCTTGGATATTCACGAAACACTAGGTTGCTCTTGCAC	1633

Db	1293	GAAGAAGGATTCTTCAAGCGTACCTTGGATATTCACGGAACACATPAGGGTTGCTCTTCAC	1352
Qy	1634	ACTCAAGTCTCGATTTCAGCAATTCGTTAAAGTGCACGGAACTGCTTTTCATCCTTAAACCA	1693
Db	1353	ACTCAAGTCTCGATTTCAGCAATTCGTTAAAGTGCACGGGAACTGCTTTTCATCCTTAAACCA	1412
Qy	1694	AAAGTAAACAGTGCTTAAATAAACTTTACCGCCATACCAAGATGTTCCAGATAAATAT	1753
Db	1413	AAAGTAAACAGTGCTTAAATAAACTTTACCGCCATACCAAGATGTTCCAGATAAATAT	1472
Qy	1754	TGGAAGCTATATACGTACTTTGTTTCAAAATGGGTCAATCGAGAAATATCGTCAACTGTTT	1813
Db	1473	TGGAAGCTATATACGTACTTTGTTTCAAAATGGGTCAATCGAGAAATATCGTCAACTGTTT	1532
Qy	1814	ACTAAAAATCAGTTTCATCAAGCAATGAAACACGCCAAAGTAAACAATTTAAGTACCGGTT	1873
Db	1533	ACTAAAAATCAGTTTCATCAAGCAATGAAACACGCCAAAGTAAACAATTTAAGTACCGGTT	1592
Qy	1874	ACTTATGAGCAAGTATTTGTTCTATTTTAAATAGTTATCTATTTTAAACGGAGGAATAA	1933
Db	1593	ACTTATGAGCAAGTATTTGTTCTATTTTAAATAGTTATCTATTTTAAACGGAGGAATAA	1652
Qy	1934	TTCTATCAGTTCGCTTTTGTAAATTTGAAAGTTTACAGTTTACTAAAGGGAAATGTAGATAA	1993
Db	1653	TTCTATCAGTTCGCTTTTGTAAATTTGAAAGTTTACAGTTTACTAAAGGGAAATGTAGATAA	1712
Qy	1994	ATTATTAGGTATCTACTGACAGCTTCCAGGAGCTAAAGGTTCCCTACGGCTCTTATC	2053
Db	1713	ATTATTAGGTATCTACTGACAGCTTCCAGGAGCTAAAGGTTCCCTACGGCTCTTATC	1772
Qy	2054	ATGGGAAGCTCGGATCATATGCAAGACAAAAATAAATCCGCAACAGCACCTTGAGGAAATG	2113
Db	1773	ATGGGAAGCTCGGATCATATGCAAGACAAAAATAAATCCGCAACAGCACCTTGAGGAAATG	1832
Qy	2114	GGACGAATTCGAGAAAAACCTCTTTTACGCTGGATTCATATCTAATAAGCCGTAAAGAGA	2173
Db	1833	GGACGAATTCGAGAAAAACCTCTTTTACGCTGGATTCATATCTAATAAGCCGTAAAGAGA	1892
Qy	2174	CGGGTTCAAAAAGGTTTAAATAAGGAGAGCAATCAATGCATTTAGCTAGAACTATATTT	2233
Db	1893	CGGGTTCAAAAAGGTTTAAATAAGGAGAGCAATCAATGCATTTAGCTAGAACTATATTT	1952
Qy	2234	TTTGGACAACGTGGAGAAATTTAGAGAACGTGCTCTCCAAGCAGGTTTACAAAGAGTAGT	2293
Db	1953	TTTGGACAACGTGGAGAAATTTAGAGAACGTGCTCTCCAAGCAGGTTTACAAAGAGTAGT	2012
Qy	2294	GCATAACATATTTTACGCTTAAAGTGTGGAACTGTAATATGGAAGAGCC	2353
Db	2013	GCATAACATATTTTACGCTTAAAGTGTGGAACTGTAATATGGAAGAGCC	2072
Qy	2354	GTAGAAGATTTAAAGCAAGAGGAGAAATTTAGAGAGATTTAATGCCATATCGTGGCCG	2413
Db	2073	GTAGAAGATTTAAAGCAAGAGGAGAAATTTAGAGAGATTTAATGCCATATCGTGGCCG	2132
Qy	2414	TTAGGATGGGAACATATCAATTTTCTTGGAGATAAATAATTTGAAGGATTCATGACACT	2473
Db	2133	TTAGGATGGGAACATATCAATTTTCTTGGAGATAAATAATTTGAAGGATTCATGACACT	2192
Qy	2474	GGGCAATGAAATTTACGTCTTACGTATAAAAGAGCGTTTTTATCTTAATAATAACGGC	2533
Db	2193	GGGCAATGAAATTTACGTCTTACGTATAAAAGAGCGTTTTTATCTTAATAATAACGGC	2252
Qy	2534	TCTTTTTATAGAAAAATTCCTTAGCTGGTTTTTTTCCGAAATGCTGGCGGTACCCCAAG	2593
Db	2253	TCTTTTTATAGAAAAATTCCTTAGCTGGTTTTTTTCCGAAATGCTGGCGGTACCCCAAG	2312
Qy	2594	AATTTAGAAATCAGTAGATCAAAATTTTTCAGATAGAAATCAGGAAATCAGATCCAAACCA	2653
Db	2313	AATTTAGAAATCAGTAGATCAAAATTTTTCAGATAGAAATCAGGAAATCAGATCCAAACCA	2372
Qy	2654	TAAAAACACTAGAACAAATTTGCAAGTTAACTAACTCAACGCTAGTAGTGGATTTAATCC	2713

Db	2373	TAAAAACA	CTAGAA	CAAAATTTGCAAAAGTTAACTAACTCAACGCTAGTAGTGGAATTTAATCC	2433
Qy	2714	CAAAATGAGCC	CAACAGAAACCGAGAGCCAGAAACAGAAATCAGAAACAAAGTAACATTCGATTTAG	2773	
Db	2433	CAAAATGAGCC	CAACAGAAACCGAGAGCCAGAAACAGAAATCAGAAACAAAGTAACATTCGATTTAG	2492	
Qy	2774	AAATGGAAGA	AGAAAAAGCAATTCAGTTCTGTGTGAATAATGCGACGAAATCGTTGCTTTATT	2833	
Db	2493	AAATGGAAGA	AGAAAAAGCAATTCAGTTCTGTGTGAATAATGCGACGAAATCGTTGCTTTATT	2552	
Qy	2834	TTTTTTTT	AAAAAGCGGTACTAGATATAACGAAACACACGAACTGAATAGAGAAACGAAAAA	2893	
Db	2553	TTTTTTTT	AAAAAGCGGTACTAGATATAACGAAACACACGAACTGAATAGAGAAACGAAAAA	2612	
Qy	2894	GAGCCATGACA	CAATTTATAAAATGTTTCAGCACATTTTATAAATGTCATAGCCCGATAAGA	2953	
Db	2613	GAGCCATGACA	CAATTTATAAATGTTTCAGCACATTTTATAAATGTCATAGCCCGATAAGA	2672	
Qy	2954	TTGCCAAACCA	ACCGCTTATCAGTTAGTTCAGATGAACTCTTCCTCCGTAGAAAGTTATTTA	3013	
Db	2673	TTGCCAAACCA	ACCGCTTATCAGTTAGTTCAGATGAACTCTTCCTCCGTAGAAAGTTATTTA	2732	
Qy	3014	ATTTAACTTT	TGTTTGAAGACGGTATATAACCGTACTATCATTTATATAGGGAATTCAGAGAG	3073	
Db	2733	ATTTAACTTT	TGTTTGAAGACGGTATATAACCGTACTATCATTTATATAGGGAATTCAGAGAG	2792	
Qy	3074	TTTTCAAGTAT	CTAAGCTACTGAAATTTAAGAAATTTGTTAAGCAATCAATTCGGAATCGTTT	3133	
Db	2793	TTTTCAAGTAT	CTAAGCTACTGAAATTTAAGAAATTTGTTAAGCAATCAATTCGGAATCGTTT	2852	
Qy	3134	GATTGCTTTTT	TGTTTCAATTTATAGAAGGTGGAGTTTGTATGAATCATATGAATGTA	3193	
Db	2853	GATTGCTTTTT	TGTTTCAATTTATAGAAGGTGGAGTTTGTATGAATCATATGAATGTA	2912	
Qy	3194	AAACTTATATA	AAAAATAGTTTATTTGGAGATAGAAGAAATTAGCAAAATCTATATACACTAG	3253	
Db	2913	AAACTTATATA	AAAAATAGTTTATTTGGAGATAGAAGAAATTAGCAAAATCTATATACACTAG	2972	
Qy	3254	AAACGTTTTA	GAAAGAGGTAGAAAGAGAAATATCTACTTTAGAAACAAAAATCAGATAAGT	3313	
Db	2973	AAACGTTTTA	GAAAGAGGTAGAAAGAGAAATATCTACTTTAGAAACAAAAATCAGATAAGT	3032	
Qy	3314	ATTTTTCTTC	GGAGGGGAAGATTATATATATAAGTTAATAGAAAAATAACAAATAATTT	3373	
Db	3033	ATTTTTCTTC	GGAGGGGAAGATTATATATATAAGTTAATAGAAAAATAACAAATAATTT	3092	
Qy	3374	ATTCGATTAT	GGAAGAAAAATTCGACTTATAGAAAGAAAAATCTTTTCAAAACATGCAA	3433	
Db	3093	ATTCGATTAT	GGAAGAAAAATTCGACTTATAGAAAGAAAAATCTTTTCAAAACATGCAA	3152	
Qy	3434	TATTGAAACAG	TTTGAATTCGAAAAAGCAAAACCAAGTTAAATTTAAACCAACTATTTATAGGAT	3493	
Db	3153	TATTGAAACAG	TTTGAATTCGAAAAAGCAAAACCAAGTTAAATTTAAACCAACTATTTATAGGAT	3212	
Qy	3494	TTATAGAAAG	GAGAACAGCTGAAATGAAATATCCCTTTTGTGTAGAAACATGTGCTTCATG	3553	
Db	3213	TTATAGAAAG	GAGAACAGCTGAAATGAAATATCCCTTTTGTGTAGAAACATGTGCTTCATG	3272	
Qy	3554	ACGCTTGT	TAAAGTACAAATTTAAAAATAGTAAAAATTCGCTCAATCTACTACCAAGCCAG	3613	
Db	3273	ACGCTTGT	TAAAGTACAAATTTAAAAATAGTAAAAATTCGCTCAATCTACTACCAAGCCAG	3332	
Qy	3614	GTAAGCAAG	AGGGGCTATTTTTCGGTATCGCTCAAAAATCAAGCATGATTTGGCGGTCGTG	3673	
Db	3333	GTAAGCAAG	AGGGGCTATTTTTCGGTATCGCTCAAAAATCAAGCATGATTTGGCGGTCGTG	3392	
Qy	3674	GTGTGTCT	CGACTTCCGAGGAGCGATTACAGAAATCAAGNATCATTTTACACATTGGA	3733	
Db	3393	GTGTGTCT	CGACTTCCGAGGAGCGATTACAGAAATCAAGNATCATTTTACACATTGGA	3452	
Qy	3734	CACCCAACT	GTATTCGTTATGGAACGCTATGCACACGAAAAACCGTTTCATACACGAAGGAC	3793	
Db	3453	CACCCAACT	GTATTCGTTATGGAACGCTATGCACACGAAAAACCGTTTCATACACGAAGGAC	3512	

QY	2301	ACATAATTATTAAAGCTATAGTGTGGAACTGTATATATATGGAAAAAGCGTGAAG	2360	QY	3381	TAGTGGAAAAAATTGACTTATTAAGGAAAAAATCTTTTCAAAAATGCAATATTGAA	3440
DB	2035	ACATATATTAAGCTATAGTGTGGAACTGTATATATGGAAAAAGCGTGAAG	2094	DB	3115	TAGTGGAAAAAATTGACTTATTAAGGAAAAAATCTTTTCAAAAATGCAATATTGAA	3174
QY	2361	AATTAAAGCAAGAGGAATTTAGAGAAATTTAATGGCATATGCGTGGCGCTTAGGAT	2420	QY	3441	ACAGTTGAATGAAAAAGCAAAACCAAGTTAATTAACCAACCTATTATTATAGGATTATAGG	3500
DB	2095	AATTAAAGCAAGAGGAATTTAGAGAAATTTAATGGCATATGCGTGGCGCTTAGGAT	2154	DB	3175	ACAGTTGAATGAAAAAGCAAAACCAAGTTAATTAACCAACCTATTATTATAGGATTATAGG	3234
QY	2421	GGGAACATATCAATTTCTTGGAGAAATACAAATTTGAAGATTACATGACACTGGGCAAA	2480	QY	3501	AAAGAGAAACAGCTGAATGAATATCCCTTTTGTGTAGAACTGCTTCTCATGACGCTT	3560
DB	2155	GGGAACATATCAATTTCTTGGAGAAATACAAATTTGAAGATTACATGACACTGGGCAAA	2214	DB	3235	AAAGAGAAACAGCTGAATGAATATCCCTTTTGTGTAGAACTGCTTCTCATGACGCTT	3294
QY	2481	TGAATTTACGTCCTTTACGTTAAGAAAGCGGTTTATCTTAAATAAAGCGCTCTTTT	2540	QY	3561	GTTAAAGTACAAATTTAAATAATAGTAAATTTGGTCTCAATCACTACCAAGCCAGGTAAG	3620
DB	2215	TGAATTTACGTCCTTTACGTTAAGAAAGCGGTTTATCTTAAATAAAGCGCTCTTTT	2274	DB	3295	GTTAAAGTACAAATTTAAATAATAGTAAATTTGGTCTCAATCACTACCAAGCCAGGTAAG	3354
QY	2541	ATAGAAAAATCCTTAGCGTGGTTTCTTCCGAAATGCTGCGTACCCCAAGATTAGA	2600	QY	3621	CAAGGGGCTATTTTGGCTCAAAATCAAGCATGATTTGCGGTCGTGCTGTTGT	3680
DB	2275	ATAGAAAAATCCTTAGCGTGGTTTCTTCCGAAATGCTGCGTACCCCAAGATTAGA	2334	DB	3355	CAAGGGGCTATTTTGGCTCAAAATCAAGCATGATTTGCGGTCGTGCTGTTGT	3414
QY	2601	AATGAGTAGATCAAAATTTACCAATAGAAATCAGGAAATCAGATCCAAACCATAAAAAC	2660	QY	3681	TCGTGACTTCCGAGGAAGCGATTCAAGAAAAATCAAGATACTTTACATTTGCAACCCCAA	3740
DB	2335	AATGAGTAGATCAAAATTTACCAATAGAAATCAGGAAATCAGATCCAAACCATAAAAAC	2394	DB	3415	TCGTGACTTCCGAGGAAGCGATTCAAGAAAAATCAAGATACTTTACATTTGCAACCCCAA	3474
QY	2661	ACTAGAACAAATTCGAAAGTTAACTACTCAACCTAGTAGTGAATTTAATCCCAATGA	2720	QY	3741	CGTTTATCGTTATGGAACGTATGACAGCAAAACCGTTTCATACAGAAAGACATTTCTGA	3800
DB	2395	ACTAGAACAAATTCGAAAGTTAACTACTCAACCTAGTAGTGAATTTAATCCCAATGA	2454	DB	3475	CGTTTATCGTTATGGAACGTATGACAGCAAAACCGTTTCATACAGAAAGACATTTCTGA	3534
QY	2721	GCCAAACAGAACGAGGACAGAAACAGAAATCAGAAATCAAGTAACTGGATTAGAAATGGA	2780	QY	3801	AAACAATTTAAGACAAATCAATACCTCTTTTATGATTTTGTATTTGATATTTACACGGCAAAAGA	3860
DB	2455	GCCAAACAGAACGAGGACAGAAACAGAAATCAGAAATCAAGTAACTGGATTAGAAATGGA	2514	DB	3535	AAACAATTTAAGACAAATCAATACCTCTTTTATGATTTTGTATTTGATTTACACGGCAAAAGA	3594
QY	2781	AGAAGAAAAAGCAATGCTGCTGTTGAATTAATGCAAGAAATCGTTGCTTTATTTT	2840	QY	3861	AACTATTTTACGCAAGCGATATTTTAAACACCGCTATTGATTTAGGTTTATGCTTACTAT	3920
DB	2515	AGAAGAAAAAGCAATGCTGCTGTTGAATTAATGCAAGAAATCGTTGCTTTATTTT	2574	DB	3595	AACTATTTTACGCAAGCGATATTTTAAACACCGCTATTGATTTAGGTTTATGCTTACTAT	3654
QY	2841	AAAACGGTATCTAGATATTAACGAAACAGCAACTGAATAGAAACGAAAAAGAGCCAT	2900	QY	3921	GATTATCAAAATCTGATAAAGGTTATCAAGCATATTTTGTGTTTGTAGAAACCGCAGTCTATGT	3980
DB	2575	AAAACGGTATCTAGATATTAACGAAACAGCAACTGAATAGAAACGAAAAAGAGCCAT	2634	DB	3655	GATTATCAAAATCTGATAAAGGTTATCAAGCATATTTTGTGTTTGTAGAAACCGCAGTCTATGT	3714
QY	2901	GACACATTTATAAAATGTTGACGCAATTTTAAATGCAATAGCCCGATAGATGCGCAA	2960	QY	3981	GACTTCAAAATCAGAAATTTAAATCTGTCAAAAGCAGCAAAATAATTTTCGCAAAATATCCG	4040
DB	2635	GACACATTTATAAAATGTTGACGCAATTTTAAATGCAATAGCCCGATAGATGCGCAA	2694	DB	3715	GACTTCAAAATCAGAAATTTAAATCTGTCAAAAGCAGCAAAATAATTTTCGCAAAATATCCG	3774
QY	2961	ACCAACGCTTATCAGTTAGTACAGTAACTCTCCCTCGTAAAGATTATTTAATTAAT	3020	QY	4041	AGAAATTTTGGAAAGTCTTTGCCAGTTGATCTAATTAACCGTAAATCAATTTTGGTATGCTCG	4100
DB	2695	ACCAACGCTTATCAGTTAGTACAGTAACTCTCCCTCGTAAAGATTATTTAATTAAT	2754	DB	3775	AGAAATTTTGGAAAGTCTTTGCCAGTTGATCTAATTAACCGTAAATCAATTTTGGTATGCTCG	3834
QY	3021	TTGTTTGAAGCGGTATATAACCGTACTATCATTTATATATAGGAAATCAGAGAGTTTCAA	3080	QY	4101	CATACCAAGAACGGAATGATAGAAATTTTGTGATCTAATTAACCGTAAATCTTTTCAAAAGA	4160
DB	2755	TTGTTTGAAGCGGTATATAACCGTACTATCATTTATATATAGGAAATCAGAGAGTTTCAA	2814	DB	3835	CATACCAAGAACGGAATGATAGAAATTTTGTGATCTAATTAACCGTAAATCTTTTCAAAAGA	3894
QY	3081	GTATCTAGCTACTGAATTTAAGATTGTTAAGCAATCAATCGGAATCGTTTCAATGCT	3140	QY	4161	ATGGCAAGATTGGTCTTTTCAAAACAAACAGATTAATAGGGCTTTTACTCGTTCAAGTCTAAC	4220
DB	2815	GTATCTAGCTACTGAATTTAAGATTGTTAAGCAATCAATCGGAATCGTTTCAATGCT	2874	DB	3895	ATGGCAAGATTGGTCTTTTCAAAACAAACAGATTAATAGGGCTTTTACTCGTTCAAGTCTAAC	3954
QY	3141	TTTTTTGTATTCATTTATAGAGGTGGAGTTTGTATGAATCATGATGAATGTAAACCTTA	3200	QY	4221	GGTTTTAAGCGGTACAGAGGCAAAACAAACAGTATGAACTCGTCTTTTAACTCTTATTT	4280
DB	2875	TTTTTTGTATTCATTTATAGAGGTGGAGTTTGTATGAATCATGATGAATGTAAACCTTA	2934	DB	3955	GGTTTTAAGCGGTACAGAGGCAAAACAAACAGTATGAACTCGTCTTTTAACTCTTATTT	4014
QY	3201	TATAAAAAATAGTTTATGGAGATAGAAATTTAGCAATATCTATACACTAGAAACGTT	3260	QY	4281	GCACGAAACGAAATTTTTCAGGAGAAAGGGTTTAAATAGGGCGTAAATAACGTCATCTTAC	4340
DB	2935	TATAAAAAATAGTTTATGGAGATAGAAATTTAGCAATATCTATACACTAGAAACGTT	2994	DB	4015	GCACGAAACGAAATTTTTCAGGAGAAAGGGTTTAAATAGGGCGTAAATAACGTCATCTTAC	4074
QY	3261	TAAGAAAGAGTTAGAAAAAGAGAAATCTACTTTAGAAACAAATCAGATAAGTATTTTC	3320	QY	4341	CCTCTCTTTAGCTACTCTTTAGTTTCAAGGCTATTTCAATCGAAACGTCGGAATATAATGTT	4400
DB	2995	TAAGAAAGAGTTAGAAAAAGAGAAATCTACTTTAGAAACAAATCAGATAAGTATTTTC	3054	DB	4075	CCTCTCTTTAGCTACTCTTTAGTTTCAAGGCTATTTCAATCGAAACGTCGGAATATAATGTT	4134
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				QY	4461	AAGTGGCTATTCAGAAAACTATCAGGGGCTAATAGGGGCTAATACCATTTCTTTTGCAA	4520

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RESULT 10
 ABS99019/c
 ID ABS99019 standard; DNA; 3765 BP.
 XX
 AC ABS99019;
 XX
 DT 18-DEC-2002 (first entry)
 XX
 DE Enterococcus faecalis contig sequence #287.
 XX
 KW Computer readable medium; Enterococcus faecalis; microbe; growth;
 KW pathogenicity; vaccine; resistance; Enterococcal infection; commercial;
 KW therapeutic; industrial; fermenting; sugar source; metabolite; vaccine;
 KW biotech technology; antibacterial; modulator of nucleic acid expression;
 KW contig; ds.
 XX
 OS Enterococcus faecalis.
 XX
 PN US2002120116-A1.
 XX
 PD 29-AUG-2002.
 XX
 PF 04-MAY-1998; 98US-00070927.
 XX
 PR 04-MAY-1998; 98US-00070927.
 XX
 PA (KUNS/) KUNSCH C A.
 PA (DILL/) DILLON P J.
 PA (BARA/) BARASH S.
 XX
 PI Kunsch CA, Dillon PJ, Barash S;
 XX
 WIPI; 2002-750065/81.
 XX
 CC Computer readable medium having recorded on it a Enterococcus faecalis
 CC nucleotide sequence useful for detecting diseases related to Enterococcus
 CC infections in animals.
 XX
 PS Claim 1; Page; 119pp; English.
 XX
 CC The present invention relates to a new computer readable medium with an
 CC Enterococcus faecalis nucleotide sequence. The invention is useful to
 CC diagnose the presence of E.faecalis in a sample or determining the
 CC presence of a specific microbe in a sample. The invention is also useful
 CC for modulating the growth or pathogenicity of E.faecalis, in a vaccine to
 CC confer resistance to Enterococcal infection, for commercial, therapeutic
 CC and industrial purposes, and for fermenting a particular sugar source or
 CC to produce a particular metabolite. The invention is useful for detecting
 CC diseases related to Enterococcus infections in animals, and for detecting
 CC E.faecalis using biotech technology. The present nucleic acid sequence
 CC represents an Enterococcus faecalis contig DNA sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from USPIO
 CC at http.sequedata.uspio.gov
 XX
 SQ Sequence 3765 BP; 1172 A; 681 C; 638 G; 1263 T; 0 U; 11 Other;

Best Local Similarity 96.6%; Pred. No. 3.5e-277; Matches 1485; Conservative 2; Mismatches 49; Indels 2; Gaps 2;			
QY	3488	TAGGATTTATAGGAACGAGAACAGCTGAATGAATATCCCTTTTGTGTAGAACTGTGC	3547
Db	2075	TAATTTTCGTAAGAAAGGAGAACAGCTGAATGAATATCCCTTTTGTGTAGAACTGTGC	2016
QY	3548	TTCAATGACGGCTTGTAAAGTACAAAATTTAAATAATAGTAAAAATCGCTCAATCACTACCA	3607
Db	2015	TTCAATGACGGCTTGTAAAGTACAAAATTTAAATAATAGTAAAAATCGCTCAATCACTACCA	1956
QY	3608	AGCCAGGTAAAGCAAAAGGGGCTATTTTTCGGTATCGCTCAAAATCAAGCATGATGGCG	3667
Db	1955	AGCCAGGTAAAGCAAAAGGGGCTATTTTTCGGTATCGCTCAAAATCAAGCATGATGGCG	1896
QY	3668	GTGCTGTGTGTCTTCACATTCGAGGAGCGATTCAGAAAAATCAAGATACATTTACAC	3727
Db	1895	GACGTGCGGTGTCTGACATTCGAGAGAGCGATTCAGAAAAATCAAGATACATTTACGC	1836
QY	3728	ATTGACACCCCAACGTTTATCGTTATGGAACGATGATGACGAGAAACCGTTCATACCGA	3787
Db	1835	ATTGACACCCCAACGTTTATCGTTATGGAACGATGATGACGAGAAACCGTTCATACCGA	1776
QY	3788	AGGACATCTGAAAAAATTAAGACAAATCAATACCTTCTTTATGATTTTATATTC	3847
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QY	3848	ACAGGCAAAAGAAACATTTTCAGCAACGATATTTTAAACACCGCTATTTGATTTAGGTT	3907
Db	1715	ACAGGCAAAAGAAACATTTTCAGCAACGATATTTTAAACACAGCTATTTGATTTAGGTT	1656
QY	3908	TTATGCTACTATGATTCATCAATCTGATAAAGTTATCAAGCATATTTTGTTTTGAAGA	3967
Db	1655	TTATGCTACTATGATTCATCAATCTGATAAAGTTATCAAGCATATTTTGTTTTGAAGA	1596
QY	3968	CGCCAGTCTATGTGACTTCAAAATCAGAAATTTAAATCTGCAAGCAGCCAAAATATTT	4027
Db	1595	CGCCAGT-TATGTGACTTCAAAATCAGAAATTTAAATCTGCAAGCAGCC-AAATATCT	1538
QY	4028	CGCAAAATATCGAGAAATATTTTGGAAAGTCTTTGCGAGTTGATCTAAAGTGAATCAAT	4087
Db	1537	CGCAAAATATCGAGAAATATTTTGGAAAGTCTTTGCGAGTTGATCTAAAGTGAATCAAT	1478
QY	4088	TTGCTATTTGCTCCATACCAAGACGACATAGAAATTTTGTATTTTATCTTAAATACCGTT	4147
Db	1477	TTGGAGTGTGCTATACCAAGACGACATAGAAATTTTGTATTTTATCTTAAATACCGTT	4118
QY	4148	ATTCTTTCAAAGAAATGCAAGATTTGCTTTTCAAACAAACAGATAATAAGGGCTTTACTC	4207
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QY	4208	GTTCAAGTCTAACGGTTTTAAGCGGTACAGAGCAAAACAAAGTAGATGAACCTGCT	4267
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QY	4268	TTAATCTCTTATTCAGCAAAACGAAATTTTTCAGGAGAAAGGCTTTAATAGGGCGTAATA	4327
Db	1297	TTAATCTCTTATTCAGCAAAACGAAATTTTTCAGGAGAAAGGCTTTAATAGGGCGTAATA	1238
QY	4328	ACGTCATGTTTACCTCTCTTTAGCCTACCTTTAGTTCAGGCTATTCATCAAGCAAAACGTCGG	4387
Db	1237	ACGTCATGTTTACCTCTCTTTAGCCTACCTTTAGTTCAGGCTATTCATCAAGCAAAACGTCGG	1178
QY	4388	AATATAATATGTTTGAAGTTTAAATCGATTCAGTCAACCTTTAGAGAAAGAGTAA	4447
Db	1177	AATATAATATGTTTGAAGTTTAAATCGATTCAGTCAACCTTTAGAGAAAGAGTAA	1118
QY	4448	TCAAATTTGTAGAGTGCCTATTTCAGAAAACTATCAAGGGGCTAATAGGGAATACATTA	4507
Db	1117	TCAAATTTGTAGAGTGCCTATTTCAGAAAACTATCAAGGGGCTAATAGGGAATACATTA	1058
QY	4508	CCATCTTTCGCAAGCTTGGGTATCAAGTCAATTAACAGTAAAGATTTATTTGTCGGTC	4567

Db	1057	CCATCTTTTGCACAAAGCTTGGGTATCAAGTGAATTTTAAACAGTAAGATTTATTTGTCGGTC	998
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Db	997	AAGGTGTTTAAATTTCAAGAAAAAAGAAAGCAAGCTCAACGTTGTTTATTTGTCAGAAAT	938
QY	4628	CGAAAGAAAGATTTAATGCTTATATTAGCGAAAAAGCAATGATATACAAAGCCTTATTTAG	4687
Db	937	CGAAAGAAAGATTTAATGCTTATATTAGCGAAAAAGCAATGATATACAAAGCCTTATTTAG	878
QY	4688	TGACGACCAAAAAAGAGATTTAGAGAGTGTAGGCAATTCCTGAAAGGACATTAGATAAAT	4747
Db	877	TGACGACCAAAAAAGAGATTTAGAGAGTGTAGGCAATTCCTGAGCGGACATTTAGATAAAT	818
QY	4748	TGCTCAAGTACTGAAAGCGCAATCAAGAAATTTTCTTTAAGATTTAAACAGGAAGAAATG	4807
Db	817	TGCTCAAGTACTGAAAGCGCAATCAAGAAATTTTCTTTAAGATTTAAACAGGAAGAAATG	758
QY	4808	GTGGCATTCAACTTCTGCTAGTGTAAATCATTTGCTATCGATCATTTAAAGTAAAGAAAG	4867
Db	757	GTGGCATTCAACTTCTGCTAGTGTAAATCATTTGCTATCGATCATTTAAAGTAAAGAAAG	698
QY	4868	AGAAAGAAAGAGCTATATAAGGCGCTGACAAATTTCTTTGACCTAGAGCATACATCA	4927
Db	697	AGAAAGAAAGAGCTATATAAGGCGCTGACAAATTTCTTTGACCTAGAGCATACATCA	638
QY	4928	TTCAAGAGACTTTAAACAGCTAGCAGAACCGCTTAAACCGGACACACAACTCGATTTGT	4987
Db	637	TTCAAGAGACTTTAAACAGCTAGCAGAACCGCTTAAACCGGACACACAACTCGATTTGT	578
QY	4988	TTAGCTATGATACAGGCTGAAAAATTAACCCGCACTAT	5025
Db	577	TTAGCTATGATACAGGCTGAAAAATAGATAAAGTCOGTAT	540
RESULT 11			
AA90954			
ID	AA90954	standard; DNA; 10323 BP.	
XX	AA90954;		
XX	17-JAN-2000	(first entry)	
DE	Plant transformation binary vector, plasmid pDAB1542.		
KW	Palmitate-CoA delta-9 desaturase; PCA; palmitic acid; desaturate; palm; modification; saturate oil; fatty acid; maize; soybean; construct; promoter regulatory element; ubiquitin promoter; transfection; coconut; maize globulin promoter; transcriptional terminator sequence; sunflower; seed embryo cell; host plant; safflower; transgenic plant; binary vector; sense orientation; plasmid pDAB1542; high level expression; ds.		
OS	Agrobacterium tumefaciens.		
OS	Escherichia coli.		
OS	Cauliflower mosaic virus.		
XX	Synthetic.		
PH	Key	Location/Qualifiers	
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FT		/note= "Correspond to bases 602-1184 of plasmid pri-15955 derived from A.tumefaciens"	
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FT	misc_feature	580..597	
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FT		/note= "Remnants of cloning manipulations"	
FT	transposon	598..2027	
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FT 2028..2062
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FT 2081..2793
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FT 4175..4272
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CC	introduced in transformed plants. MARs are located in non-transcribed	
CC	regions of genes and form the physical boundaries of individual DNA	
CC	loops. They are rich in adenosine and thymine bases and contain certain	
CC	conserved sequence elements and structural features. They are about 300-	
CC	2000 bp in length. Increased levels of expression of DNA introduced into	
CC	plants can be achieved by use of MAR. They can also reduce the position	
CC	effect in transgenic organisms. The present DNA sequence is the	
CC	Arabidopsis transformation binary vector pARCTAF-Bin, identical to the	
CC	vector pARCT2-Bin, except that it contains a MAR dimer-2 positioned 5' to	
CC	the Act2 transcription initiation region and the MAR dimer-1 positioned	
CC	3' to the nos 3' UTR (untranslated region). This vector is used to test	
CC	the two orientations of the artificial MAR dimer in Arabidopsis	
XX		
Sequence 17111 BP; 4720 A; 3952 C; 4065 G; 4371 T; 0 U; 3 Other;		
Query Match	20.2%; Score 1111; DB 3; Length 17111;	
Best Local Similarity	100.0%; Pred. No. 3.2e-212;	
Matches 1111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	936	AAACGAAAACGAATGATACACCATCAGTCGAAAAGAGATATAATGGGAGATAAGAC 995
DB	5745	AAAGAAAACGAATGATACACCATCAGTCGAAAAGAGATATAATGGGAGATAAGAC 5804
QY	996	GGTTCGTGTTTCGTGCTGACATTGCACCATATCATATAAAATCGAAACAGAAAGATGGCGG 1055
DB	5805	GGTTCGTGTTTCGTGCTGACATTGCACCATATCATATAAAATCGAAACAGAAAGATGGCGG 5864
QY	1056	AAACGTAAGAGAGTATGGAATPAGACTTAGAGCAAACTTTAGAGTGTGTTGATAGT 1115
DB	5865	AAACGTAAGAGAGTATGGAATPAGACTTAGAGCAAACTTTAGAGTGTGTTGATAGT 5924
QY	1116	GCAGTATCTTAAAAATTTTGTTATATAGGAATTCGAGTTAAATTAGATGCTAAAAATTGT 1175
DB	5925	GCAGTATCTTAAAAATTTTGTTATATAGGAATTCGAGTTAAATTAGATGCTAAAAATTGT 5984
QY	1176	AATTAAGAGAGGTGATTCATGAGCAAAAAATATAAAATATTCTCAAACTTTTTAACGA 1235
DB	5985	AATTAAGAGAGGTGATTCATGAGCAAAAAATATAAAATATTCTCAAACTTTTTAACGA 6044
QY	1236	GTGAAAAGTACTCAACCAATATATAAACAAATTTGAATTTTAAAGAAACCGATCCGTTT 1295
DB	6045	GTGAAAAGTACTCAACCAATATATAAACCAATTTGAATTTTAAAGAAACCGATCCGTTT 6104
QY	1296	ACGAAATTTGGAACAGGTAAAGGGCATTTAACGACGAAACTGGCTAAAAATAAGTAAACAGG 1355
DB	6105	ACGAAATTTGGAACAGGTAAAGGGCATTTAACGACGAAACTGGCTAAAAATAAGTAAACAGG 6164
QY	1356	TAACGCTATTGAATPAGACAGTCTATTGCACTTATCGTCAGAAAAATTTAAACTGA 1415
DB	6165	TAACGCTATTGAATPAGACAGTCTATTGCACTTATCGTCAGAAAAATTTAAACTGA 6224
QY	1416	ATACTCGTGTCACATTAAATCACCAGATATCTACAGTTCAAATTCCTAACCAAAACAGA 1475
DB	6225	ATACTCGTGTCACATTAAATCACCAGATATCTACAGTTCAAATTCCTAACCAAAACAGA 6284
QY	1476	GGTATAAAATTTGGGAGTATCCTTACATTTAAGACACAAATTTATTTAAAAAGTGG 1535
DB	6285	GGTATAAAATTTGGGAGTATCCTTACCATTTTAAGCACACAAATTTATTTAAAAAGTGG 6344
QY	1536	TTTTTTGAAGCCATGCGCTGACATCTATCTGATGTTGCAAGAAGGATTTCTACAAGGCTA 1595
DB	6345	TTTTTTGAAGCCATGCGCTGACATCTATCTGATGTTGCAAGAAGGATTTCTACAAGGCTA 6404
QY	1596	CCTTCGGATATTCAACGAACTAGGGTTGCTTTGCACACTCAAGTCTCGATTCAGCAAT 1655
DB	6405	CCTTCGGATATTCAACGAACTAGGGTTGCTTTGCACACTCAAGTCTCGATTCAGCAAT 6464
QY	1656	TGCTTTAAGCTGCCAGCGAATGCTTTTCACTCCTAAACCAAAAGTAAACAGTGTCTTAATA 1715
DB	6465	TGCTTTAAGCTGCCAGCGAATGCTTTTCACTCCTAAACCAAAAGTAAACAGTGTCTTAATA 6524
QY	1716	AACTTTACCGGCCATACACAGATGTTCCAGATAAAATTTTGGAAAGCTATATACGTACTTGT 1775

5525	AACTTACCCGCCATACACAGATGTTCCAGATAAATATTGGAAGCTATATACGTACTTTTG	6558
1776	TTTCAAAATGGGTCAATCGGAATATCGTCAACTGTTTACTTAAAAATCAGTTTCATCAAG	1835
6585	TTTCAAAATGGGTCAATCGGAATATCGTCAACTGTTTACTTAAAAATCAGTTTCATCAAG	6644
1836	CAATGAAACACGCCAAAGTAAACAAATTTAAGTACCGTTACTTATGAGCAAGTATTGTCTA	1895
6645	CAATGAAACACGCCAAAGTAAACAAATTTAAGTACCGTTACTTATGAGCAAGTATTGTCTA	6704
1896	TTTTTTAATAGTTATCTATTATTTTAACGGGAGGAAATAAATPCTATGAGTCGCTTTGTAAA	1955
6705	TTTTTTAATAGTTATCTATTATTTTAACGGGAGGAAATAAATPCTATGAGTCGCTTTGTAAA	6764
1956	TTTGGAAAGTACACGTTACTTAAAGGGAATGTAGATAAAATTTATTAGTATACTACTGACA	2015
6765	TTTGGAAAGTACACGTTACTTAAAGGGAATGTAGATAAAATTTATTAGTATACTACTGACA	6824
2016	GCYTCCAAGGAGCTAAAGAGGTCCTTAGCGC	2046
6825	GCYTCCAAGGAGCTAAAGAGGTCCTTAGCGC	6855
RESULT 13		
AAAD01290		
ID	AAAD01290	standard; DNA; 17116 BP.
XX	AAAD01290;	
XX	12-OCT-2000	(first entry)
XX	Arabidopsis transformation binary vector, pAct2Af-bin.	
XX	Matrix Attachment Region; MAR; scaffold attachment region; pAct2Af-bin;	
XX	Arabidopsis transformation binary vector; gene expression;	
XX	transgenic organism; ds.	
XX	Synthetic.	
XX	Key	Location/Qualifiers
XX	misc_feature	64..709
FT	/*tag= a	
FT	/note= "Corresponds to nucleotides 1-646 of MAR dimer-1"	
FT	4044..4689	
FT	/*tag= b	
FT	/note= "Corresponds to nucleotides 1-646 of MAR dimer-3"	
XX	WO200032800-A1.	
XX	08-JUN-2000.	
XX	30-NOV-1999;	99WO-US028123.
XX	01-DEC-1998;	98US-0110437P.
XX	(DOWC) DOW AGROSCIENCES LLC.	
XX	Van Der Geest AHM, Ainley WM, Cowen NM, Welter ME, Woosley AT;	
XX	WPI; 2000-412345/35.	
XX	An isolated DNA molecule for use as a matrix attachment region to	
XX	increase expression of genes introduced in transformed plants comprises a	
XX	298 base pair sequence described in the specification.	
XX	Example 3; Page 64-68; 73pp; English.	
XX	The patent discloses a DNA molecule, useful as matrix attachment region	
XX	(MAR) or scaffold attachment region, to increase the expression of genes	
XX	introduced in transformed plants. MARs are located in non-transcribed	
XX	regions of genes and form the physical boundaries of individual DNA	
XX	loops. They are rich in adenosine and thymine bases and contain certain	
XX	conserved sequence elements and structural features. They are about 300-	

CC 2000 bp in length. Increased levels of expression of DNA introduced into
CC plants can be achieved by use of MAR. They can also reduce the position
CC effect in transgenic organisms. The present DNA sequence is the
CC Arabidopsis transformation binary vector pA2TAF-bin, identical to the
CC vector pA2T-bin, except that it contains a MAR dimer-1 positioned 5' to
CC the Act2 transcription initiation region and the MAR dimer-3 positioned
CC 3' to the nos 3' UTR (untranslated region). This vector is used to test
CC the two orientations of the artificial MAR in Arabidopsis
XX
SQ Sequence 17116 BP; 4686 A; 3968 C; 4052 G; 4407 T; 0 U; 3 Other;
Query Match 20.2%; Score 1111; DB 3; Length 17116;
Best Local Similarity 100.0%; Pred. No. 3.2e-212;
Matches 1111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 936 ARAAGAAACGAAATGATACACCATCATGTCGCAAAAGAGATATATCGGAGATAGAC 995
DB 5750 ARAAGAAACGAAATGATACACCATCATGTCGCAAAAGAGATATATCGGAGATAGAC 5809
QY 996 GGTTCGTGTTGCTGCTGACATTCACCATATCATATAAATCGAAACAGCAAGAAATGGCGG 1055
DB 5810 GGTTCGTGTTGCTGCTGACATTCACCATATCATATAAATCGAAACAGCAAGAAATGGCGG 5869
QY 1056 AAGCTGAAAGAGATTGATGAAATAGACTTAGAAGCAAACTTAAGAGTGTGTATAGT 1115
DB 5870 AAGCTGAAAGAGATTGATGAAATAGACTTAGAAGCAAACTTAAGAGTGTGTATAGT 5929
QY 1116 GCAGTATCTTAAATTTGATATAGTAATGCAATTAATTAAGTGTGCTAAATTTGT 1175
DB 5930 GCAGTATCTTAAATTTGATATAGTAATGCAATTAATTAAGTGTGCTAAATTTGT 5989
QY 1176 AATTAAGAGGAGTATCATGAACAAATAATAAATATCTCAAACTTTTAAACGA 1235
DB 5990 AATTAAGAGGAGTATCATGAACAAATAATAAATATCTCAAACTTTTAAACGA 6049
QY 1236 GTGAAAGTACTCAACCAATATTAACCAATTAATTAAGTGTGCTAAATTTGT 1295
DB 6050 GTGAAAGTACTCAACCAATATTAACCAATTAATTAAGTGTGCTAAATTTGT 6109
QY 1296 ACGAAATTTGAACAGGTAAAGGGCATTTAAGCAAGAACTGGCTAAATTAAGTAAACAGG 1355
DB 6110 ACGAAATTTGAACAGGTAAAGGGCATTTAAGCAAGAACTGGCTAAATTAAGTAAACAGG 6169
QY 1356 TAAGCTGATTTGAATAGACAGTCACTATTAACCTATGCTGAGAAATTAAGTAACTGA 1415
DB 6170 TAAGCTGATTTGAATAGACAGTCACTATTAACCTATGCTGAGAAATTAAGTAACTGA 6229
QY 1416 ATACTCGTGTCACTTTAATTTCAACAGATATTTCAAGTTTCAATTCCTTAACAAACAGA 1475
DB 6230 ATACTCGTGTCACTTTAATTTCAACAGATATTTCAAGTTTCAATTCCTTAACAAACAGA 6289
QY 1476 GGTATAAATTTGTTGGAGTATTCCTTAACAGTATTTCAACAGTATTTAATAAAGTGG 1535
DB 6290 GGTATAAATTTGTTGGAGTATTCCTTAACAGTATTTCAACAGTATTTAATAAAGTGG 6349
QY 1536 TTTTGAAGCCATGCTGCTGACATCTATCTGATTTGTAAGAGGATTTCAACAGGTA 1595
DB 6350 TTTTGAAGCCATGCTGCTGACATCTATCTGATTTGTAAGAGGATTTCAACAGGTA 6409
QY 1596 CTTTGGATTTTCCCGAAGTATGCTTCTTGACACTCAAGTCTCGATTGACCAAT 1655
DB 6410 CTTTGGATTTTCCCGAAGTATGCTTCTTGACACTCAAGTCTCGATTGACCAAT 6469
QY 1656 TGCTTAAGCTGCCAGCGGAATGCTTTCATCTTAACCAAGTATTAACAGTGTCTTAATA 1715
DB 6470 TGCTTAAGCTGCCAGCGGAATGCTTTCATCTTAACCAAGTATTAACAGTGTCTTAATA 6529
QY 1716 AACTTACCGCCATPACCAAGATTTCCAGATAAATTTGGAAGTATATACGTTGTTG 1775
DB 6530 AACTTACCGCCATPACCAAGATTTCCAGATAAATTTGGAAGTATATACGTTGTTG 6589
QY 1776 TTTCAAAATGGTCAATCGAGATATCGTCAACTGTTTACTAAAATCAAGTTTCATCAAG 1835

DB 6590 TTTCAAAATGGTCAATCGAGATATCGTCAACTGTTTACTAAAAATCAGTTTCATCAAG 6649
QY 1836 CAATGAACACGCCAAAGTAAACATTTAAGTACCGTTACTATGAGCAAGTATTGCTA 1895
DB 6650 CAATGAACACGCCAAAGTAAACATTTAAGTACCGTTACTATGAGCAAGTATTGCTA 6709
QY 1896 TTTTAAATAGTATCTATTTAATTTAAGCGGAGGAAATTAATTTATGAGTCGCTTTGTA 1955
DB 6710 TTTTAAATAGTATCTATTTAATTTAAGCGGAGGAAATTAATTTATGAGTCGCTTTGTA 6769
QY 1956 TTTGAAAGTTACAGTTTACTTAAAGGGAATAGATAAATTTATGAGTATCTACTGACA 2015
DB 6770 TTTGAAAGTTTACAGTTTACTTAAAGGGAATAGATAAATTTATGAGTATCTACTGACA 6829
QY 2016 GCTTCCAAAGGAGCTAAAGAGGTCCTTAGCGC 2046
DB 6830 GCTTCCAAAGGAGCTAAAGAGGTCCTTAGCGC 6860
RESULT 14
ABK98591/c
ID ABK98591 standard; DNA; 10929 BP.
XX AC ABK98591;
XX DT 07-AUG-2003 (revised)
XX DT 21-OCT-2002 (first entry)
DE pEP25 vector fragment containing Xylr/Xylo/CP25 sequences.
XX ds; promoter; gram positive bacteria; fusion promoter; T5; CP25; P32;
KW P59; P1P2; PL; xylO; tetO; trpO; malO; lambdaclO; cellular proliferation;
KW antibiotic; vector.
XX Eubacteria.
OS Bacteriophage lambda.
OS Escherichia coli.
OS Synthetic.
XX WO200251982-A2.
XX PN 04-JUL-2002.
XX PD 21-DEC-2001; 2001WO-US050250.
PP 27-DEC-2000; 2000US-0259434P.
PR 06-SEP-2001; 2001US-00948993.
XX (ELIT-) ELITRA PHARM INC.
XX PI Haselbeck R, Wall D, Gross M;
XX WPI; 2002-575374/61.
XX Isolated nucleic acid comprises bacterial promoters modified to have
PT altered activity in at least one gram-positive organism, e.g. Bacillus
PT anthracis or Clostridium botulinum, useful for regulating gene expression
PT in bacteria.
XX Example 1; Page 202-205; 246pp; English.
XX The invention relates to an isolated nucleic acid comprising a fusion
XX promoter comprising at least one promoter that is modified to have
XX altered activity in at least one gram-positive organism, or comprising
XX T5, CP25, P32, P59, P1P2 or PL linked to at least one operator consisting
XX of xylO, tetO, trpO, malO or lambdaclO, where at least one operator is
XX positioned so binding of a repressor to an operator represses
XX transcription from the fusion promoter. Also included are vectors and
XX host cells comprising the fusion promoters, a method of identifying genes
XX involved in cellular proliferation or required for proliferation of a
XX prokaryotic cell using the vector, a method of identifying compounds that
XX inhibit the proliferation of a prokaryotic cell using the vector, a
XX method of identifying a compound that reduces the activity or level of a

CC the nucleic acid. The fusion promoter is useful for identifying genes
 CC involved in cellular proliferation, identifying a compound that reduces
 CC the activity or level of a gene product required for proliferation of a
 CC cell, inhibiting the activity or expression of a gene in an operon
 CC required for proliferation, manufacturing an antibiotic, identifying a
 CC gene that is required for proliferation of a prokaryotic cell,
 CC identifying a compound that inhibits the proliferation of a prokaryotic
 CC cell and regulating gene expression in bacteria. The present sequence is
 CC a plasmid containing a fusion promoter of the invention
 XX
 SQ Sequence 10929 BP; 3259 A; 2175 C; 2157 G; 3338 T; 0 U; 0 Other;
 Query Match 20.2%; Score 1109.4; DB 8; Length 10929;
 Best Local Similarity 99.9%; Pred. No. 6e-212;
 Matches 1110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 936 AAAAGAAAAACGAAATGATACCAATCAGTGCAGAAAAAGATATAATGGAGATAAGAC 995
 DB 5830 AAAAGAAAAACGAAATGATACCAATCAGTGCAGAAAAAGATATAATGGAGATAAGAC 5771
 QY 996 GGTTCGTGTTGCTGCTGACCTGCACCATATCATATAAATCGAACACGCAAGATCGCG 1055
 DB 5770 GGTTCGTGTTGCTGCTGACCTGCACCATATCATATAAATCGAACACGCAAGATCGCG 5711
 QY 1056 AAACGTAAAAAGAGTTATGGAATAGACTTAGAACCAACTTAAAGAGTGTGTGATAGT 1115
 DB 5710 AAACGTAAAAAGAGTTATGGAATAGACTTAGAACCAACTTAAAGAGTGTGTGATAGT 5651
 QY 1116 GCAGTATCTTAAATTTTGTATATAGGAATGGAATTAATAGATCTAAAAATTTGT 1175
 DB 5650 GCAGTATCTTAAATTTTGTATATAGGAATGGAATTAATAGATCTAAAAATTTGT 5591
 QY 1176 AATTAAGAGAGGTGATTACATCAACAAAAATATAAATATTCTCAAACTTTTAAACGA 1235
 DB 5590 AATTAAGAGAGGTGATTACATCAACAAAAATATAAATATTCTCAAACTTTTAAACGA 5531
 QY 1236 GTGAAAAAGTACTCAACCAATATAAACAATTTAAAGAAACCGATACCGTTT 1295
 DB 5530 GTGAAAAAGTACTCAACCAATATAAACAATTTAAAGAAACCGATACCGTTT 5471
 QY 1296 ACCGAATTTGGAACAGGTAAAGGCACTTTAAGCAGCAATCGCTGCTAAATTAAGTAACAG 1355
 DB 5470 ACCGAATTTGGAACAGGTAAAGGCACTTTAAGCAGCAATCGCTGCTAAATTAAGTAACAG 5411
 QY 1356 TAACGTCTATTGAATTAGACAGTCATCTATTCAACTTATCGTCAGAAAAAATTAACACTGA 1415
 DB 5410 TAACGTCTATTGAATTAGACAGTCATCTATTCAACTTATCGTCAGAAAAAATTAACACTGA 5351
 QY 1416 ATACTCGTGTCACTTTAATTCACCAAGATATCTACAGTTTCAATTCCTTACCAACACAGA 1475
 DB 5350 ATACTCGTGTCACTTTAATTCACCAAGATATCTACAGTTTCAATTCCTTACCAACACAGA 5291
 QY 1476 GGTATAAAATTTGTTGGAGTATTCCTTACCATTAAAGCACACAAATTTAAAAAAGTGG 1535
 DB 5290 GGTATAAAATTTGTTGGAGTATTCCTTACCATTAAAGCACACAAATTTAAAAAAGTGG 5231
 QY 1536 TTTTGTAAAGCCATGCGCTGACATCTATCTGATTTGTTGAAGAGGATTTCTACAGCGTA 1595
 DB 5230 TTTTGTAAAGCCATGCGCTGACATCTATCTGATTTGTTGAAGAGGATTTCTACAGCGTA 5171
 QY 1596 CCTTGGATATTTCACGGAACACTAGGTTGCTTTCGACACTCAAGTCTCGATTTCGCAAT 1655
 DB 5170 CCTTGGATATTTCACGGAACACTAGGTTGCTTTCGACACTCAAGTCTCGATTTCGCAAT 5111
 QY 1656 TGCTTAAGCTGCCAGCGGAATGCTTTTCATCTAAACCAAAAGTAAACAGTGTCTTAATAA 1715
 DB 5110 TGCTTAAGCTGCCAGCGGAATGCTTTTCATCTAAACCAAAAGTAAACAGTGTCTTAATAA 5051
 QY 1716 AACTTACCCGCCATACACAGATGTTCCAGATATAATTTGGAAGCTATATACGACTTTG 1775
 DB 5050 AACTTACCCGCCATACACAGATGTTCCAGATATAATTTGGAAGCTATATACGACTTTG 4991
 QY 1776 TTTCAAAATGGGTCAATCGAGAAATATCGTCAACTGTGTTTACTAAAAATCAGTTTTCATCAAG 1835

Search completed: September 1, 2004, 15:00:05
 Job time : 1900 secs

DB 4990 TTTCAAAATGGTCAATCGAATATCGTCACTGTTTACTAAAAATCAGTTTCATCAAG 4931
 QY 1836 CAATGAAACACGCCAAAGTAAACAAATTTAAGTACCGTTTACTTATGAGCAAGTATTGTCTA 1895
 DB 4930 CAATGAAACACGCCAAAGTAAACAAATTTAAGTACCGTTTACTTATGAGCAAGTATTGTCTA 4871
 QY 1896 TTTTAAATAGTTATCTATTATTAAACGGGAGGAATAATTTCTATGAGTCGCTTTTGTAAA 1955
 DB 4870 TTTTAAATAGTTATCTATTATTAAACGGGAGGAATAATTTCTATGAGTCGCTTTTGTAAA 4811
 QY 1956 TTTGAAAAATTTACAGCTTACTTAAAGGGAATGTAGATAAATTTATTAGGTATCTACTGACA 2015
 DB 4810 TTTGAAAAATTTACAGCTTACTTAAAGGGAATGTAGATAAATTTATTAGGTATCTACTGACA 4751
 QY 2016 GCTTCCAAAGGAGCTAAAGAGTCCCTAGCGC 2046
 DB 4750 GCTTCCAAAGGAGCTAAAGAGTCCCTAGCGC 4720

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OM nucleic - nucleic search, using sw model

Run on: September 1, 2004, 14:22:19 ; Search time 336 Seconds
(without alignments)
9079.063 Million cell updates/sec

Title: US-10-030-390-2

Perfect score: 5497

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Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA:*
- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4994.4	90.9	5217	4	US-09-100-703A-25
2	4993.4	90.8	5230	4	US-09-100-703A-26
3	4944.6	90.0	5231	4	US-09-100-703A-27
4	1111	20.2	10323	4	US-09-280-428A-11
5	884	16.1	6243	2	US-09-056-075-1
6	737.2	13.4	783	4	US-09-134-000C-3303
7	731.6	13.3	738	2	US-08-743-637B-193
8	273.2	5.0	1167	4	US-09-134-000C-3296
9	247.2	4.5	696	4	US-09-134-000C-3315
10	244.2	4.4	3792	2	US-08-992-334-1
11	244.2	4.4	3792	3	US-08-302-752-1
12	244.2	4.4	5234	2	US-08-992-334-2
13	244.2	4.4	5234	3	US-08-302-752-2
14	244.2	4.4	5313	4	US-09-329-920-1
15	244.2	4.4	6169	2	US-08-875-154-2
16	244.2	4.4	6722	2	US-08-992-334-3
17	244.2	4.4	6722	3	US-08-302-752-3
18	244.2	4.4	10216	2	US-08-875-154-1
19	241	4.4	735	2	US-08-743-637B-194
20	240.8	4.4	720	4	US-09-107-532A-982
21	229.2	4.2	732	2	US-08-743-637B-192
22	223.2	4.1	2964	3	US-08-886-819A-18
23	223.2	4.1	2964	3	US-08-980-357-18
24	223.2	4.1	3190	2	US-08-286-819A-30
25	223.2	4.1	3190	3	US-08-980-357-30
26	223.2	4.1	10851	2	US-08-886-819A-16
27	223.2	4.1	10851	3	US-08-980-357-16

28	191	3.3	204	4	US-09-134-000C-3302	Sequence 3302, App
29	143.2	2.6	384	1	US-08-040-753-1	Sequence 1, Appl
30	143.2	2.6	5502	4	US-09-702-705-785	Sequence 785, App
31	143.2	2.6	5502	4	US-09-736-457-785	Sequence 785, App
32	143.2	2.6	5502	4	US-09-614-124B-785	Sequence 785, App
33	143.2	2.6	5502	4	US-09-671-325-785	Sequence 785, App
34	143.2	2.6	5502	4	US-09-589-184-785	Sequence 785, App
35	142	2.6	142	4	US-09-060-878-1	Sequence 1, Appl
36	141.6	2.6	2220	2	US-08-864-224-1	Sequence 1, Appl
37	140.8	2.6	4557	4	US-08-778-717-5	Sequence 5, Appl
38	140.8	2.6	6363	4	US-08-929-967-6	Sequence 6, Appl
39	140	2.5	7659	3	US-09-128-314-3	Sequence 4, Appl
40	140	2.5	8157	3	US-09-128-314-3	Sequence 4, Appl
C 41	139.6	2.5	6361	3	US-08-646-538-7	Sequence 7, Appl
C 42	139.6	2.5	6361	3	US-09-503-222-7	Sequence 7, Appl
43	139.6	2.5	6727	2	US-08-125-462-2	Sequence 2, Appl
44	139.6	2.5	6727	2	US-08-891-848-2	Sequence 2, Appl
45	139.6	2.5	6799	2	US-08-125-462-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-100-703A-25
; Sequence 25, Application US/09100703A
; Patent No. 6610300
; GENERAL INFORMATION:
; APPLICANT: SEGERS, Ruud PAM
; APPLICANT: WATERFIELD, Nicolas R
; APPLICANT: FRANDSEN, Peer L
; APPLICANT: WELLS, Jeremy M.
; TITLE OF INVENTION: COLISTRIDIMUM PERFRINGENS VACCINE
; FILE REFERENCE: 97288 US
; CURRENT APPLICATION NUMBER: US/09/100,703A
; CURRENT FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: EP9701889.1
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 5217
; TYPE: DNA
; ORGANISM: Clostridium perfringens
US-09-100-703A-25

Query Match	90.9%	Score 4994.4	DB 4	Length 5217
Best Local Similarity	99.9%	Pred. No. 0		
Matches 4998	Conservative	0	Mismatches	6
			Indels	0
			Gaps	0
QY	494	TTCTAACTAGTAGATCCGGCTGCTTAAAGCCGGAAGGAGCTGAGTTGGCTGCTGCC	553	
DB	214	TCCAAATGATCAGATCCGGCTGCTTAAAGCCGGAAGGAGCTGAGTTGGCTGCTGCC	273	
QY	554	ACCGCTGAGCAATACTAGCATACCCCTGGGGCTCTAAACGGCTCTTCAAGGGGTTTT	613	
DB	274	ACCGCTGAGCAATACTAGCATACCCCTGGGGCTCTTAAAGGGGTTTTGAGGGGTTTT	333	
QY	614	TTGCTGAAAGGAGGAACCTATATCCGGATACCTCGAGCAAGCTCTAGAAATCGATACGAT	673	
DB	334	TTGCTGAAAGGAGGAACCTATATCCGGATACCTCGAGCAAGCTCTAGAAATCGATACGAT	393	
QY	674	TTTGAAGTGGCAACAGATATAAAGGAGGTTTAAATTTGTTGCTGACTTTTAAACAA	733	
DB	394	TTTGAAGTGGCAACAGATATAAAGGAGGTTTAAATTTGTTGCTGACTTTTAAACAA	453	
QY	734	GCAATACAAATCATTTGTCGCAACAGATAGCGACAGAGGCGGAAAAACATTCCTGGTGG	793	
DB	454	GCAATACAAATCATTTGTCGCAACAGATAGCGACAGAGGCGGAAAAACATTCCTGGTGG	513	
QY	794	ATCATTGATAAGCAATGCTTTTCTAAAGATATAAAGCTATAAAGCTATGATCAAT	853	
DB	514	ATCATTGATAAGCAATGCTTTTCTAAAGATATAAAGCTATAAAGCTATGATCAAT	573	

QY 854 AGTTTAGAAAAGATGTGATCCGTAGCGGTTTTCAAAATTTGCAACCGAGAAATCAATTC 913
 DB 574 AGTTTAGAAAAGATGTGATCCGTAGCGGTTTTCAAAATTTGCAACCGAGAAATTC 633
 QY 914 TATCCCTTTTATCAAGAAGCCCAAAAGAAAACGAATGATACACCAATCAGTGCRAAAA 973
 DB 634 TATCCCTTTTATCAAGAAGCCCAAAAGAAAACGAATGATACACCAATCAGTGCRAAAA 693
 QY 974 AAGATATAATCGGAGATAAGACGGTTCTGTGTTCTGTCTGCTGCTGCACCATATCATAAAA 1033
 DB 694 AAGATATAATCGGAGATAAGACGGTTCTGTGTTCTGTCTGCTGCTGCACCATATCATAAAA 753
 QY 1034 TCGAAACAGCAAGAAATGCGCGAAACGTAAGAAAGTATGGAATTAAGACTTAGAAGCA 1093
 DB 754 TCGAAACAGCAAGAAATGCGCGAAACGTAAGAAAGTATGGAATTAAGACTTAGAAGCA 813
 QY 1094 AACTTAGAGTGTGTTGATGTGAGTGTGAGTATCTTAAATTTTGTATAATAGAAATTTGAAGTT 1153
 DB 814 AACTTAGAGTGTGTTGATGTGAGTGTGAGTATCTTAAATTTTGTATAATAGAAATTTGAAGTT 873
 QY 1154 AAAATTAGATGCTAAAAATTTGTAATTAAGAAAGGAGTATCATGAAACAAAAATATAAAA 1213
 DB 874 AAAATTAGATGCTAAAAATTTGTAATTAAGAAAGGAGTATCATGAAACAAAAATATAAAA 933
 QY 1214 TATCTCAAAATTTTAAACGAGTGAAGAAAGTATCTCAACCAATATAAACAATTAAGT 1273
 DB 934 TATCTCAAAATTTTAAACGAGTGAAGAAAGTATCTCAACCAATATAAACAATTAAGT 993
 QY 1274 TTAAGAAACCGATACCGTTTACGAATTCGAACAGGTAAAGGCGATTTAAACGACGAAA 1333
 DB 994 TTAAGAAACCGATACCGTTTACGAATTCGAACAGGTAAAGGCGATTTAAACGACGAAA 1053
 QY 1334 CTGGCTAAAAATTAAGTAACAGGTAAACGTTTAACTGTAATTAAGTAACTATCAACTTA 1393
 DB 1054 CTGGCTAAAAATTAAGTAACAGGTAAACGTTTAACTGTAATTAAGTAACTATCAACTTA 1113
 QY 1394 TCGTCAGAAAAATTAAGTAACAGGTAAACGTTTAACTGTAATTAAGTAACTATCAACTTA 1453
 DB 1114 TCGTCAGAAAAATTAAGTAACAGGTAAACGTTTAACTGTAATTAAGTAACTATCAACTTA 1173
 QY 1454 TTCAATTTCCCTAACAAACAGAGGTATAAAATTTGTTGGAGTATTCCTTACCAATTAAGC 1513
 DB 1174 TTCAATTTCCCTAACAAACAGAGGTATAAAATTTGTTGGAGTATTCCTTACCAATTAAGC 1233
 QY 1514 ACACAAATTTAAAGAAAGTGGTTTTGAAAGCCATCGCTGACATCTATCTGATGTT 1573
 DB 1234 ACACAAATTTAAAGAAAGTGGTTTTGAAAGCCATCGCTGACATCTATCTGATGTT 1293
 QY 1574 GAAAGAGGATTTCAAGCGTACCTTGGATATTCAACGAAACACTAGGTTGCTCTTCAC 1633
 DB 1294 GAAAGAGGATTTCAAGCGTACCTTGGATATTCAACGAAACACTAGGTTGCTCTTCAC 1353
 QY 1634 ACTCAAGTCTCGATTACAGAAATTTGTTAAAGTGGTAAAGTGGTAAAGTGGTAAAGTGGT 1693
 DB 1354 ACTCAAGTCTCGATTACAGAAATTTGTTAAAGTGGTAAAGTGGTAAAGTGGTAAAGTGGT 1413
 QY 1694 AAAGTAAACAGTGTCTTAATAAAGTAACTACCGCCCATACCAAGATGTTCCAGATAAATAT 1753
 DB 1414 AAAGTAAACAGTGTCTTAATAAAGTAACTACCGCCCATACCAAGATGTTCCAGATAAATAT 1473
 QY 1754 TGGAGCTATATACGTAATTTGTTTCAAAATTTGTTTCAAAATTTGTTTCAAAATTTGTTT 1813
 DB 1474 TGGAGCTATATACGTAATTTGTTTCAAAATTTGTTTCAAAATTTGTTTCAAAATTTGTTT 1533
 QY 1814 ACTAAAAATCAGTTTCAATCAAGCAATGAAACAGCGCAAGTAAACAAATTTAAGTACCGTT 1873
 DB 1534 ACTAAAAATCAGTTTCAATCAAGCAATGAAACAGCGCAAGTAAACAAATTTAAGTACCGTT 1593
 QY 1874 ACTTAGAGCAAGTATGTTTATTTTAAAGTATCTATTTAAGTATCTATTTAAGTATCTATTT 1933
 DB 1594 ACTTAGAGCAAGTATGTTTATTTTAAAGTATCTATTTAAGTATCTATTTAAGTATCTATTT 1653

QY 1934 TTCTATGATGCTGCTTTTGTAAATTTGGAAGTTTACAGTTTAAAGGAATGTAGATAA 1993
 DB 1654 TTCTATGATGCTGCTTTTGTAAATTTGGAAGTTTACAGTTTAAAGGAATGTAGATAA 1713
 QY 1994 ATTATTAGTATGATGCTTCCAGAGGAGTAAAGAGGTCCTTAGCGCTCTTATC 2053
 DB 1714 ATTATTAGTATGATGCTTCCAGAGGAGTAAAGAGGTCCTTAGCGCTCTTATC 1773
 QY 2054 ATFGGGAAGCTCGGATCATATGCAAGACAAATTAACCTCGCAACAGCACTTGGAGAAATG 2113
 DB 1774 ATFGGGAAGCTCGGATCATATGCAAGACAAATTAACCTCGCAACAGCACTTGGAGAAATG 1833
 QY 2114 GGACGAATCGGAAACCCCTTTTACGCTGGATTACATATCTAATAAAGCCGTAAAGAGA 2173
 DB 1834 GGACGAATCGGAAACCCCTTTTACGCTGGATTACATATCTAATAAAGCCGTAAAGAGA 1893
 QY 2174 CGGGTTCAAAAAGGTTTAAATAAAGGAGAAAGCAATCAATGCAATAGCTAGAACTATATTT 2233
 DB 1894 CGGGTTCAAAAAGGTTTAAATAAAGGAGAAAGCAATCAATGCAATAGCTAGAACTATATTT 1953
 QY 2234 TTTGCAACAGCTGGAGAAATTTAGAGAACTGCTCTTCCAAAGCCAGTTTCAAGAGCTAGT 2293
 DB 1954 TTTGCAACAGCTGGAGAAATTTAGAGAACTGCTCTTCCAAAGCCAGTTTCAAGAGCTAGT 2013
 QY 2294 GCACCTAAACATATTAATTTTAAAGCTATAAGTGTGTGAAACACTGTATATATATGAAAAAGCC 2353
 DB 2014 GCACCTAAACATATTAATTTTAAAGCTATAAGTGTGTGAAACACTGTATATATATGAAAAAGCC 2073
 QY 2354 GTAGAGAAATTAAGAGCAAGGAGAAATTTAGAGAGAAATTTAAATGCCATATCGCTGGCCG 2413
 DB 2074 GTAGAGAAATTAAGAGCAAGGAGAAATTTAGAGAGAAATTTAAATGCCATATCGCTGGCCG 2133
 QY 2414 TTAGATGGAACATATCAATTTTCTTGGAGAAATCAAAATTTTGAAGGATTCATGACACT 2473
 DB 2134 TTAGATGGAACATATCAATTTTCTTGGAGAAATCAAAATTTTGAAGGATTCATGACACT 2193
 QY 2474 GGGCAATGAATTTTACGCTCTTACGTAATAAGAGCCGTTTATTTCTTAATAATAAGCC 2533
 DB 2194 GGGCAATGAATTTTACGCTCTTACGTAATAAGAGCCGTTTATTTCTTAATAATAAGCC 2253
 QY 2534 TCTTTTATAGAAAAATTCCTTTAGCGTGTGTTTTTCCGAAATGCTGCGGTACCCCAAG 2593
 DB 2254 TCTTTTATAGAAAAATTCCTTTAGCGTGTGTTTTTCCGAAATGCTGCGGTACCCCAAG 2313
 QY 2594 AATTAGAAATGATAGATCAAAATTTTACGAAATAGATTCAGAAATTCAGAAATTCAGATCCAAACA 2653
 DB 2314 AATTAGAAATGATAGATCAAAATTTTACGAAATAGATTCAGAAATTCAGATCCAAACA 2373
 QY 2654 TAAACACACTGAAACAAATTTGCAAAAGTTAACTCAACGCTAGTGTAGTTTAATTC 2713
 DB 2374 TAAACACACTGAAACAAATTTGCAAAAGTTAACTCAACGCTAGTGTAGTTTAATTC 2433
 QY 2714 CAAATGAGCCAAACAGAACCCAGAGCCAGAAACAGAAATCAGAAATTCAGATTTAG 2773
 DB 2434 CAAATGAGCCAAACAGAACCCAGAGCCAGAAACAGAAATCAGAAATTCAGATTTAG 2493
 QY 2774 AAATGGAAGAAAGAAAGCAATGCTGCTGTAATTAATGCAACCAATTCGTTGCTTAT 2833
 DB 2494 AAATGGAAGAAAGAAAGCAATGCTGCTGTAATTAATGCAACCAATTCGTTGCTTAT 2553
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 DB 2554 TTTTAAAAAGCGGTATATAGATATAACGAAAAACAGAACTGAATAGAAACGAAAAA 2613
 QY 2894 GAGCCATGACATTTATTAATTTTGNCGCAATTTTATTAATGCAATGCCGATAGA 2953
 DB 2614 GAGCCATGACATTTATTAATTTTGNCGCAATTTTATTAATGCAATGCCGATAGA 2673
 QY 2954 TTGCCAAAAACAGCTTATCAGTTAGTCAAGTAACTCTTCCCTCGTAAAGATTATTTA 3013
 DB 2674 TTGCCAAAAACAGCTTATCAGTTAGTCAAGTAACTCTTCCCTCGTAAAGATTATTTA 2733
 QY 3014 ATTPAACTTTGTTGAAGCGGTATATATACCGTACTATCAATATATATAGGGAATCAGAGAG 3073

Db 2734 ATTAACCTTGTGTTGAAGACGGTATATAACCGTACTATCATATATAGGAAATCAGAGAG 2793
Qy 3074 TTTTCAAGTACTTAAGCTACTGAATTTAAGAAATTTAAGCAATCAATCGGAATCGTTT 3133
Db 2794 TTTTCAAGTACTTAAGCTACTGAATTTAAGAAATTTAAGCAATCAATCGGAATCGTTT 2853
Qy 3134 GATTGCTTTTGTATTTCAATTTATAGAAGTGGAGTTTGTATGAATCATGATGAATGTA 3193
Db 2854 GATTGCTTTTGTATTTCAATTTATAGAAGTGGAGTTTGTATGAATCATGATGAATGTA 2913
Qy 3194 AAACCTATATAAATAATAGTTTATTTAGAGATAGAAATTTAGCAATATCTATACACTAG 3253
Db 2914 AAACCTATATAAATAATAGTTTATTTAGAGATAGAAATTTAGCAATATCTATACACTAG 2973
Qy 3254 AAACGTTTAAAGAAAGAGTTAGAAAGAGAAATCTACTTTAGAAACAAATTCAGATAAGT 3313
Db 2974 AAACGTTTAAAGAAAGAGTTAGAAAGAGAAATCTACTTTAGAAACAAATTCAGATAAGT 3033
Qy 3314 ATTTTCTTCGGAGGGGAGAT 3373
Db 3034 ATTTTCTTCGGAGGGGAGAT 3093
Qy 3374 ATTCGATTAGTGGAAAAAATTTGACTTTATAAGGAAAAAATCTTTTCAAAAATGCAAA 3433
Db 3094 ATTCGATTAGTGGAAAAAATTTGACTTTATAAGGAAAAAATCTTTTCAAAAATGCAAA 3153
Qy 3434 TATTGAAACAGTTGAATGAATAAGCAAAACCAAGTTAATTAATAAACAACCTATTTATAGAT 3493
Db 3154 TATTGAAACAGTTGAATGAATAAGCAAAACCAAGTTAATTAATAAACAACCTATTTATAGAT 3213
Qy 3494 TTATAGAAAGGAGAACAGCTGAATGAATATCCCTTTTGTGTAGAAACCTGCTTCATG 3553
Db 3214 TTATAGAAAGGAGAACAGCTGAATGAATATCCCTTTTGTGTAGAAACCTGCTTCATG 3273
Qy 3554 ACGCTTTGTTAAAGTACAAATTTAAATAATAGTAAATTCGCTCAATCACTACCAAGCCAG 3613
Db 3274 ACGCTTTGTTAAAGTACAAATTTAAATAATAGTAAATTCGCTCAATCACTACCAAGCCAG 3333
Qy 3614 GTAAAGCAAGGGCTATTTTTCGCTATCGCTCAAAATCAAGCATGATTCGGCTCGTG 3673
Db 3334 GTAAAGCAAGGGCTATTTTTCGCTATCGCTCAAAATCAAGCATGATTCGGCTCGTG 3393
Qy 3674 GTGTGTCTTCACTTCGAGGAAACGATTCAGAAATCAAGATAATTTACACATTGGA 3733
Db 3394 GTGTGTCTTCACTTCGAGGAAACGATTCAGAAATCAAGATAATTTACACATTGGA 3453
Qy 3734 CACCAACGTTTATCGTTATGGAACGTTATGGAACGTAACCGTTTATACACGAAAGGAC 3793
Db 3454 CACCAACGTTTATCGTTATGGAACGTTATGGAACGTAACCGTTTATACACGAAAGGAC 3513
Qy 3794 ATTCTGAAACAAATTTAAGACAAATCAATACCTTCTTTATTTGATTTGATATTTACACGG 3853
Db 3514 ATTCTGAAACAAATTTAAGACAAATCAATACCTTCTTTATTTGATTTGATATTTACACGG 3573
Qy 3854 CAAAAGAACTATTTACGCAAGCGATATTTTAAACACCGCTATTTAGTTTATGCTATGC 3913
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Qy 3914 CTACTATGATTTCAATCTGATAAGGTTATCAAGCATATTTGTTTATAGAAACCGCAG 3973
Db 3634 CTACTATGATTTCAATCTGATAAGGTTATCAAGCATATTTGTTTATAGAAACCGCAG 3693
Qy 3974 TCTATGTGACTTCAAAATCAGAAATTTAAATCTCTGCAAGCAGCCAAATTAATTTCCGAAA 4033
Db 3694 TCTATGTGACTTCAAAATCAGAAATTTAAATCTCTGCAAGCAGCCAAATTAATTTCCGAAA 3753
Qy 4034 ATATCCGAGAAATTTTGGAAAGCTTTTGGCAAGTTGATCAACGCTGATATTTTGGTA 4093
Db 3754 ATATCCGAGAAATTTTGGAAAGCTTTTGGCAAGTTGATCAACGCTGATATTTTGGTA 3813
Qy 4094 TTGCTCCATACCAAGAACGCAATGTAGAAATTTTGTGATCCTAATTTACCGTTATTTCTT 4153

Db 3814 TTGCTCGCATACCAAGAACGGACAATGTAGAAATTTTGTATCTCTAATTAACCGTTATCTT 3873
Qy 4154 TCAAGAAATGGCAAGATTTGGTCTTTTCAACAAACAGATAAATAAGGCTTTTACTCGTTCAA 4213
Db 3874 TCAAGAAATGGCAAGATTTGGTCTTTTCAACAAACAGATAAATAAGGCTTTTACTCGTTCAA 3933
Qy 4214 GTCTAACGCTTTTAAAGCGGTACAGAAAGCAAAAAACAAGTAGATGAACCTCGTTTAATC 4273
Db 3934 GTCTAACGCTTTTAAAGCGGTACAGAAAGCAAAAAACAAGTAGATGAACCTCGTTTAATC 3993
Qy 4274 TCTTATTCAGAAACGAAATTTTTCAGGAGAAAGGGTTTAAATAGGGCGTAAATACGTCAC 4333
Db 3994 TCTTATTCAGAAACGAAATTTTTCAGGAGAAAGGGTTTAAATAGGGCGTAAATACGTCAC 4053
Qy 4334 TCTTATTCAGAAACGAAATTTTTCAGGAGAAAGGGTTTAAATAGGGCGTAAATACGTCAC 4393
Db 4054 TCTTATTCAGAAACGAAATTTTTCAGGAGAAAGGGTTTAAATAGGGCGTAAATACGTCAC 4113
Qy 4394 ATATGTTGAGTTTAAATATCGATTTAGATCAACCTTTAGAGAAAGAAAGAAATCAAAA 4453
Db 4114 ATATGTTGAGTTTAAATATCGATTTAGATCAACCTTTAGAGAAAGAAAGAAATCAAAA 4173
Qy 4454 TTGTTAGAAAGTCCCTATTTAGAAACTATCAAGGGCTTAAATAGGGAATACATTAACATTC 4513
Db 4174 TTGTTAGAAAGTCCCTATTTAGAAACTATCAAGGGCTTAAATAGGGAATACATTAACATTC 4233
Qy 4514 TTTGCAAGCTTTGGGTATCAAGTGAATTTAAACAGTAAAGATTTATTTGCTCGTCAAGGCT 4573
Db 4234 TTTGCAAGCTTTGGGTATCAAGTGAATTTAAACAGTAAAGATTTATTTGCTCGTCAAGGCT 4293
Qy 4574 GGTTTAAATTCAGAAAGAAAGAAAGAGACGAAACGTCACCGTTCATTTGTCAGAAATGGAAG 4633
Db 4294 GGTTTAAATTCAGAAAGAAAGAAAGAGACGAAACGTCACCGTTCATTTGTCAGAAATGGAAG 4353
Qy 4634 AAGATTTAATGGCTTATTTAGCGAAAAAAGCGATGTATACAAGCTTTATTTAGTGACGA 4693
Db 4354 AAGATTTAATGGCTTATTTAGCGAAAAAAGCGATGTATACAAGCTTTATTTAGTGACGA 4413
Qy 4694 CCARAAAGAGATTAGAAAGTCTAGGATTTCTTGAACGACATTTAGATTAATTTGCTGA 4753
Db 4414 CCARAAAGAGATTAGAAAGTCTAGGATTTCTTGAACGACATTTAGATTAATTTGCTGA 4473
Qy 4754 AGGTACTGAAGCGCAATCAGGAAATTTTCTTAAAGATTTAAACCGAGGAAATGCTGCA 4813
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Qy 4874 AAGAAAGCTATATAAGCGCTGACAAATTTCTTTGCTTAGAGCATACATTTCAAG 4933
Db 4594 AAGAAAGCTATATAAGCGCTGACAAATTTCTTTGCTTAGAGCATACATTTCAAG 4653
Qy 4934 AAGCTTTAAACAAAGCTAGCAGAACGCTTAAACCGACACACAACTCGATTTGTTAGCT 4993
Db 4654 AAGCTTTAAACAAAGCTAGCAGAACGCTTAAACCGACACACAACTCGATTTGTTAGCT 4713
Qy 4994 ATGATACAGGCTGAAATATAAAGCGCTAGTACCATTTGATTTATATCTATGATACGCTG 5053
Db 4714 ATGATACAGGCTGAAATATAAAGCGCTAGTACCATTTGATTTATATCTATGATACGCTG 4773
Qy 5054 TTTGTTTTTCTTGTCTGTTTAGCGAATGTTAGCAGAAATATACAGAGTAAGATTTTAA 5113
Db 4774 TTTGTTTTTCTTGTCTGTTTAGCGAATGTTAGCAGAAATATACAGAGTAAGATTTTAA 4833
Qy 5114 TTAATTTAGGGGAGAGAGAGAGTAGCCGAAACTTTTAGTTGCTTGGCTTGGACTGAA 5173
Db 4834 TTAATTTAGGGGAGAGAGAGAGTAGCCGAAACTTTTAGTTGCTTGGCTTGGACTGAA 4893
Qy 5174 CGAGTGAAGGAAAGGCTTACTTAAACCGTGAAGGGCGAGTAGAGCGAAGCACTTGA 5233
Db 4894 CGAGTGAAGGAAAGGCTTACTTAAACCGTGAAGGGCGAGTAGAGCGAAGCACTTGA 4953

Db	1668	TCCTATGAGTCGCTTTTGTAAATTTGGAAAGTTACACGCTTACTAAAGGGAATGTAGATAAA	1727
Qy	1995	TTATTAGGTATCTACTGACAGCTTCCAAGAGCTAAAGAGGTCCCTTAGCGCTCTTATCA	2054
Db	1728	TTATTAGGTATCTACTGACAGCTTCCAAGAGCTAAAGAGGTCCCTTAGCGCTCTTATCA	1787
Qy	2055	TGGGGAAGCTCGGATCATATATGCAAGACAAAATAAAGCTCGCAACAGCACTTGGAGAAATGG	2114
Db	1788	TGGGGAAGCTCGGATCATATGCAAGACAAAATAAAGCTCGCAACAGCACTTGGAGAAATGG	1847
Qy	2115	GAGCAATCGAGAAAAACCCCTCTTTACGCTGGATTACATATCTAATAAAGCCGTAAAGAGAC	2174
Db	1848	GAGCAATCGAGAAAAACCCCTCTTTACGCTGGATTACATATCTAATAAAGCCGTAAAGAGAC	1907
Qy	2175	GGGTTCAAAAAGGTTTAAATAAAGGAGAGCAATCAATGCATTAGCTAGAACTATATTTT	2234
Db	1908	GGGTTCAAAAAGGTTTAAATAAAGGAGAGCAATCAATGCATTAGCTAGAACTATATTTT	1967
Qy	2235	TTGGAACAAGCTGGAGAAATTTAGAGAAAGTGCTCTCCAAGACCAAGTACAAAGAGCTAGTG	2294
Db	1968	TTGGAACAAGCTGGAGAAATTTAGAGAAAGTGCTCTCCAAGACCAAGTACAAAGAGCTAGTG	2027
Qy	2295	CACATAACATAATTTAATTAACGCTATAAGTGTGTGAACACTGTATATATGAAAAAGCCG	2354
Db	2028	CACATAACATAATTTAATTAACGCTATAAGTGTGTGAACACTGTATATATGAAAAAGCCG	2087
Qy	2355	TAGAAGAAATTAAGCAAGAGGAGAAATTTAGAGNAGATTTTAATGCCATATGCGTGCCGT	2414
Db	2088	TAGAAGAAATTAAGCAAGAGGAGAAATTTAGAGNAGATTTTAATGCCATATGCGTGCCGT	2147
Qy	2415	TAGGATGGGAACATATCAATTTTCTTGGAGAAATACAAATTTGAAGGATTACATGACACTG	2474
Db	2148	TAGGATGGGAACATATCAATTTTCTTGGAGAAATACAAATTTGAAGGATTACATGACACTG	2207
Qy	2475	GGCAATGAATTTTACGTCCTTACGTTATAAAGAGCCGCTTTTATCTTTAATATAACGGCT	2534
Db	2208	GGCAATGAATTTTACGTCCTTACGTTATAAAGAGCCGCTTTTATCTTTAATATAACGGCT	2267
Qy	2535	CTTTTATAGAAAAATCCTTAGCGTGCTTTTTCGAAATGCTGCGGTACCCCAAGA	2594
Db	2268	CTTTTATAGAAAAATCCTTAGCGTGCTTTTTCGAAATGCTGCGGTACCCCAAGA	2327
Qy	2595	ATTAGAAATCAGTAGATCAAAATTTATCACGAATAGAAATCAGGAAAAATCAGATCCACCAT	2654
Db	2328	ATTAGAAATCAGTAGATCAAAATTTATCACGAATAGAAATCAGGAAAAATCAGATCCACCAT	2387
Qy	2655	AAAAACACTAGACAAATTCGAAGTTAACTTAATCAACGCTAGTAGTGATTTATCCC	2714
Db	2388	AAAAACACTAGACAAATTCGAAGTTAACTTAATCAACGCTAGTAGTGATTTATCCC	2447
Qy	2715	AAATGAGCCACAGAACAGAGCCAGAAAAAGCAATCAGAACAAAGTAACTTGGATTTAGA	2774
Db	2448	AAATGAGCCACAGAACAGAGCCAGAAAAAGCAATCAGAACAAAGTAACTTGGATTTAGA	2507
Qy	2775	AATGGAAGAGAAAAAGCAATGACTTCGTGTGTGAAATTAATGCAAGAAATCGTTGCTTATTT	2834
Db	2508	AATGGAAGAGAAAAAGCAATGACTTCGTGTGTGAAATTAATGCAAGAAATCGTTGCTTATTT	2567
Qy	2835	TTTTTTTAAAGCGGTATCTAGATATATAAGAAACAGCAACTGAATAGAAACGAAAAAG	2894
Db	2568	TTTTTTTAAAGCGGTATCTAGATATATAAGAAACAGCAACTGAATAGAAACGAAAAAG	2627
Qy	2895	AGCCATGACACATTTATAAATGTTTGACGACATTTTATAAATGATAGATAGATAGAT	2954
Db	2628	AGCCATGACACATTTATAAATGTTTGACGACATTTTATAAATGATAGATAGATAGAT	2687
Qy	2955	TGCCAAACCAACGCTTATCAGTTAGTCAGATGAACCTCTCCCTCGTAAGAAGTTATTTAA	3014
Db	2688	TGCCAAACCAACGCTTATCAGTTAGTCAGATGAACCTCTCCCTCGTAAGAAGTTATTTAA	2747
Qy	3015	TTAACTTTGTTTGAAGACCGGTATATAACCGTACTATCATTTATATAGGGAATCAGAGAGT	3074

Db	2748	TTAACTTTTGTGTAAGACGGTAATATAACCGTACTATCAITTAATATATAGGGAATCAGAGAGT	2800
Qy	3075	TTTCAAGTACTAAGCTACTGAAATTTTAAGAAATTTTAAGCAATCAATTCGGAATCGTTTG	3134
Db	2808	TTTCAAGTACTAAGCTACTGAAATTTTAAGAAATTTTAAGCAATCAATTCGGAATCGTTTG	2867
Qy	3135	ATTGCTTTTGTGTAATTCANTTATAGNAGGTGGAGTTTGTATGAATCATGATGAATGTAA	3194
Db	2868	ATTGCTTTTGTGTAATTCANTTATAGNAGGTGGAGTTTGTATGAATCATGATGAATGTAA	2927
Qy	3195	AACCTATATAAAAAATAGTTTATTTGGAGATAAGAAAAATAGCAAAATCTATACACTAGA	3254
Db	2928	AACCTATATAAAAAATAGTTTATTTGGAGATAAGAAAAATAGCAAAATCTATACACTAGA	2987
Qy	3255	AACGTTAAGAAAGAGTTAGAAAAGAGAAATATCTACTTAGAAAACAAAATCAGATAAGTA	3314
Db	2988	AACGTTTAAAGAAAGAGTTAGAAAAGAGAAATATCTACTTAGAAAACAAAATCAGATAAGTA	3047
Qy	3315	TTTTTCTTCGGAGGGGGAAGATTATATATATAAGTTAAATAGAAAATAACAAAAATAATTA	3374
Db	3048	TTTTTCTTCGGAGGGGGAAGATTATATATATAAGTTAAATAGAAAATAACAAAAATAATTA	3107
Qy	3375	TTTCGATTAGTGGAAAAAATTTGACTTATAAAGGAAAAAATCTTTTTCAAAAATCGCAAT	3434
Db	3108	TTTCGATTAGTGGAAAAAATTTGACTTATAAAGGAAAAAATCTTTTTCAAAAATCGCAAT	3167
Qy	3435	ATTGAAACAGTTCGAATCGAAAACCAACCAAGTTTAATTAACCAACCTATTTTATAGGATT	3494
Db	3168	ATTGAAACAGTTCGAATCGAAAACCAACCAAGTTTAATTAACCAACCTATTTTATAGGATT	3227
Qy	3495	TATAGGAAAGGAGAACAGCTGAAATGAATATCCCTTTTGTGTAGAAACTGTGCTTCATGA	3554
Db	3228	TATAGGAAAGGAGAACAGCTGAAATGAATATCCCTTTTGTGTAGAAACTGTGCTTCATGA	3287
Qy	3555	CGGCTTGTAAAGTACAAATTTAAATATAGTAATTCGCTCAATCACTACCAAGCCAGG	3614
Db	3288	CGGCTTGTAAAGTACAAATTTAAATATAGTAATTCGCTCAATCACTACCAAGCCAGG	3347
Qy	3615	TAAAGCAAAAGGGGCTATTTTTCGGTATCCCTCAAAATCAAGCATGATTCGGCGTGGTG	3674
Db	3348	TAAAGCAAAAGGGGCTATTTTTCGGTATCCCTCAAAATCAAGCATGATTCGGCGTGGTG	3407
Qy	3675	TGTTGTTCTGACTTCGAGGAGCGGATTCAAGAAAATCAAGATACATTTACATTTGGAC	3734
Db	3408	TGTTGTTCTGACTTCGAGGAGCGGATTCAAGAAAATCAAGATACATTTACATTTGGAC	3467
Qy	3735	ACCCAAAGTTTATCGTTATCGAATCAATACCTTCTTTATTTGATTTTGATTTACACACGGC	3794
Db	3468	ACCCAAAGTTTATCGTTATCGAATCAATACCTTCTTTATTTGATTTTGATTTACACACGGC	3527
Qy	3795	TTCTGAAAACAATTTAAGACAAATCAATACCTTCTTTATTTGATTTTGATTTACACACGGC	3854
Db	3528	TTCTGAAAACAATTTAAGACAAATCAATACCTTCTTTATTTGATTTTGATTTACACACGGC	3587
Qy	3855	AAAAGAACTATTTTCAGCAACGATTTTAAACAAACGGCTATGATTTAGTTTATGCTTATGCC	3914
Db	3588	AAAAGAACTATTTTCAGCAACGATTTTAAACAAACGGCTATGATTTAGTTTATGCTTATGCC	3647
Qy	3915	TACTATGATTATCAAAATCTGATAAAGTTATCAAGCATATTTTGTTTTGAATGAAACGGCAGT	3974
Db	3648	TACTATGATTATCAAAATCTGATAAAGTTATCAAGCATATTTTGTTTTGAATGAAACGGCAGT	3707
Qy	3975	CTATGTGACTTCAAAATCAGAAATTAATCTGTCAAAAGGCGCAAAATAATTTTCGCAAAA	4034
Db	3708	CTATGTGACTTCAAAATCAGAAATTAATCTGTCAAAAGGCGCAAAATAATTTTCGCAAAA	3767
Qy	4035	TATCCGAGAAATTTTGGAAAGTCTTTGCGAGTTGATCTAAACGCTGAATCATTTTCGTAT	4094
Db	3768	TATCCGAGAAATTTTGGAAAGTCTTTGCGAGTTGATCTAAACGCTGAATCATTTTCGTAT	3827
Qy	4095	TGCTCGCATACCAAGAACGACAAATTTTGTGATCTCTAAATTAACGGTTATTTCTTT	4154
Db	3828	TGCTCGCATACCAAGAACGACAAATTTTGTGATCTCTAAATTAACGGTTATTTCTTT	3887

QY 4155 CAAGAGATGCAAGATTGGTCTTTTCAACAACACAGATAAATAAGGGCTTTTACTCGTTCAAG 4214
DB 3888 CAAGAATGGCAAGATTGGTCTTTTCAACAACACAGATAAATAAGGGCTTTTACTCGTTCAAG 3947
QY 4215 TCTAACCGTTTTAAGCGGTACAGAGGCAAAACAAAGTAGATGAACCCCTGGTTTAACTCT 4274
DB 3948 TCTAACCGTTTTAAGCGGTACAGAGGCAAAACAAAGTAGATGAACCCCTGGTTTAACTCT 4007
QY 4275 CTTATTGACAGAAACGAAATTTTCAGAGAAAGGGTTTAAATAGGGCGTAAATACGTCAT 4334
DB 4008 CTTATTGACAGAAACGAAATTTTCAGAGAAAGGGTTTAAATAGGGCGTAAATACGTCAT 4067
QY 4335 GTTTACCCCTCTCTTTAGCGTACTTTAGTTCAAGGCTATTCAATCGAAACGTCGCAATATAA 4394
DB 4068 GTTTACCCCTCTCTTTAGCGTACTTTAGTTCAAGGCTATTCAATCGAAACGTCGCAATATAA 4327
QY 4395 TATGTTGAGTTTAAATATCGATTAGATCAACCCCTTAGAGAAAGAAAGATTAATCAAAAT 4454
DB 4128 TATGTTGAGTTTAAATATCGATTAGATCAACCCCTTAGAGAAAGAAAGATTAATCAAAAT 4187
QY 4455 TGTTAGAGTGCCTATTTCAGAAACTATCAAGGGCTAAATAGGGAATACATTACCATCT 4514
DB 4188 TGTTAGAGTGCCTATTTCAGAAACTATCAAGGGCTAAATAGGGAATACATTACCATCT 4247
QY 4515 TTGCAAGCTTTGGGTATCAAGTGAATTTAAACAGTAAAGATTTATTTGTCGTCGAAGGGT 4574
DB 4248 TTGCAAGCTTTGGGTATCAAGTGAATTTAAACAGTAAAGATTTATTTGTCGTCGAAGGGT 4307
QY 4575 GTTTAAATCAAGAAAGAAAGCGACGTCACGCTGTCATTTGTCAGATGGAAGA 4634
DB 4308 GTTTAAATCAAGAAAGAAAGCGACGTCACGCTGTCATTTGTCAGATGGAAGA 4367
QY 4635 AGATTTAATGGCTTATATTAGCGAAAGAGGATGTATACAGGCTTTATTATGTCAGCAC 4694
DB 4368 AGATTTAATGGCTTATATTAGCGAAAGAGGATGTATACAGGCTTTATTATGTCAGCAC 4427
QY 4695 CAAAAAGAGATTAGAAAGTCTAGGATTCCTGAACGACATTAAGTAAATGCTGAA 4754
DB 4428 CAAAAAGAGATTAGAAAGTCTAGGATTCCTGAACGACATTAAGTAAATGCTGAA 4487
QY 4755 GGTACTGAAGCGAATCAGGAAATTTCTTTAAGATTAAACCCAGGAAAGAAATGCTGCAT 4814
DB 4488 GGTACTGAAGCGAATCAGGAAATTTCTTTAAGATTAAACCCAGGAAAGAAATGCTGCAT 4547
QY 4815 TCAATCTGCTAGTTAAATCAATTTGCTATCGATCTTAAGTAAAGTAAAGAAAGAAAG 4874
DB 4548 TCAATCTGCTAGTTAAATCAATTTGCTATCGATCTTAAGTAAAGTAAAGAAAGAAAG 4607
QY 4875 AGAAGCTATATAAGGCGCTGACAAATTTCTTTGACTTGAAGCATACATTCAATCAAGA 4934
DB 4608 AGAAGCTATATAAGGCGCTGACAAATTTCTTTGACTTGAAGCATACATTCAATCAAGA 4667
QY 4935 GACTTTAAACAGCTAGCAGAACCGCTTAAACCGGACACAACTCGATTTGTTAGCTA 4994
DB 4668 GACTTTAAACAGCTAGCAGAACCGCTTAAACCGGACACAACTCGATTTGTTAGCTA 4727
QY 4995 TCATACAGCTGAAATTAACCCGCACTATGCCATTATCTATATCTATGATACGCTGT 5054
DB 4728 TGATACAGCTGAAATTAACCCGCACTATGCCATTATCTATATCTATGATACGCTGT 4787
QY 5055 TTGTTTTTCTTGTGTTAGCGAATGATTAGCAGAAATATACAGAGTAAAGATTTTAAAT 5114
DB 4788 TTGTTTTTCTTGTGTTAGCGAATGATTAGCAGAAATATACAGAGTAAAGATTTTAAAT 4847
QY 5115 TAAATTTAGGGGAGAGGAGTAGCCGAAACTTTTGTGCTGTCGCTGAGCTGAAC 5174
DB 4848 TAAATTTAGGGGAGAGGAGTAGCCGAAACTTTTGTGCTGTCGCTGAGCTGAAC 4907
QY 5175 GAAAGTGAGGAAAGGCTACTAAACCGTCAGGGGCGAGTGAGAGCGAAGCGAACACTTTGAT 5234
DB 4908 GAAAGTGAGGAAAGGCTACTAAACCGTCAGGGGCGAGTGAGAGCGAAGCGAACACTTTGAT 4967

QY 5235 TTTTAAATTTTCTATCTCTTTTAGTCTATTAGAGTATATCTTTATTTGCTCTATAAATCTATT 5294
DB 4968 TTTTAAATTTTCTATCTCTTTTAGTCTATTAGAGTATATCTTTATTTGCTCTATAAATCTATT 5027
QY 5295 TAGAGCATATATAGATTTTATTGAATAGTCAATTTAAGTTGAGCATATTAGAGGAGGAAAA 5354
DB 5028 TAGAGCATATATAGATTTTATTGAATAGTCAATTTAAGTTGAGCATATTAGAGGAGGAAAA 5087
QY 5355 TCTTCGAGAAATATTTTGAAGAACCCGATTACATGATTGGATTAGTCTCTTGTGTTAGCT 5414
DB 5088 TCTTCGAGAAATATTTTGAAGAACCCGATTACATGATTGGATTAGTCTCTTGTGTTAGCT 5147
QY 5415 GGTTTTTAACTAAAGTAGTAGTGAATTTTGAATTTTGGTGTGTGTCTCTTGTGTTAGTAT 5474
DB 5148 GGTTTTTAACTAAAGTAGTAGTGAATTTTGAATTTTGGTGTGTGTCTCTTGTGTTAGTAT 5207
QY 5475 TTGCTAGTCAAGTCAATTAATA 5497
DB 5208 TTGCTAGTCAAGTCAATTAATA 5230

RESULT 3
US-09-100-703A-27
; Sequence 27, Application US/09100703A
; Patent No. 6610300
; GENERAL INFORMATION:
; APPLICANT: SEGERS, Ruud PAM
; APPLICANT: WATERFIELD, Nicolas R
; APPLICANT: FRANDSEN, Peer L
; APPLICANT: WELLS, Jeremy M.
; TITLE OF INVENTION: COLISTRIDUM PERFRINGENS VACCINE
; FILE REFERENCE: 97288 US
; CURRENT APPLICATION NUMBER: US/09/100,703A
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: EP97201888.1
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 5231
; TYPE: DNA
; ORGANISM: Clostridium perfringens
US-09-100-703A-27

Query Match 90.0%; Score 4944.6; DB 4; Length 5231;
Best Local Similarity 99.6%; Pred No. 0;
Matches 4975; Conservative 0; Mismatches 4; Indels 18; Gaps 1;

QY 501 TAGTAGATCCGGCTCTCTAACAAAGCCCGAAAGAGCTGAGTTGGCTGCTGCCACCGCTG 560
DB 253 TCGCGATCCGGCTCTCTAACAAAGCCCGAAAGAGCTGAGTTGGCTGCTGCCACCGCTG 312
QY 561 ACATATACTACATAACCCCTTGGGCTCTTAACGGCTCTTAACGGCTTTTGGCTGA 620
DB 313 AGCAATACTACATAACCCCTTGGGCTCTTAACGGCTCTTAACGGCTTTTGGCTGA 372
QY 621 AAGGAGGAATCTATATCCGGATGACCTCGAGGCAAGCTCTAGAACTGATACGATTTGAAG 680
DB 373 AAGGAGGAATCTATATCCG-----ACTAGAATCGATACGATTTGAAG 414
QY 681 TGGCAACAGATATAAAGAGAGTAAATTTGTTGCTGAACCTTTTAAACAAAGCAATA 740
DB 415 TGGCAACAGATATAAAGAGAGTAAATTTGTTGCTGAACCTTTTAAACAAAGCAATA 474
QY 741 CAATCATCTCCCAACAGATAGCGACAGAGGCGGAAAAACATTGCTGTCGATCATTC 800
DB 475 CAATCATCTCGCAACAGATAGCGACAGAGGCGGAAAAACATTGCTGTCGATCATTC 534
QY 801 ATAAAGCAATGCTTTTCTAAAGATAAAGCTATATAAAGACTATGGAATCAATAGTTAG 860
DB 535 ATAAAGCAATGCTTTTCTAAAGATAAAGCTATATAAAGACTATGGAATCAATAGTTAG 594
QY 861 AAAAGATGTGATCGGTAGCGGTTTTTCAAAATTTTCAACACCGAAGTAAATTAATCTCCT 920

QY	3081	GTATCTAAGCTACTGAAATTTAAGAAATGTTAAGCAATCAATCGAAATCGTTGATTGCT	3140
Db	2815	GTATCTAAGCTACTGAAATTTAAGAAATGTTAAGCAATCAATCGAAATCGTTGATTGCT	2874
QY	3141	TTTTTTGTTATTCATTTATAGAAAGTGGAGTTTGTATGAATCATCATCAATGTAATAACTTA	3200
Db	2875	TTTTTTGTTATTCATTTATAGAAAGTGGAGTTTGTATGAATCATCATCAATGTAATAACTTA	2934
QY	3201	TATAAAAATAGTTTATTTGGAGATAAGAAAAATTAGCAAAATATCTATACACTAGAAACGTT	3260
Db	2935	TATAAAAATAGTTTATTTGGAGATAAGAAAAATTAGCAAAATATCTATACACTAGAAACGTT	2994
QY	3261	TAGAAAGAGTTAGAAAGAGAAATATCTACTTATAGAAACAAATATCAGATTAATTTTTC	3320
Db	2995	TAGAAAGAGTTAGAAAGAGAAATATCTACTTATAGAAACAAATATCAGATTAATTTTTC	3054
QY	3321	TTCCGAGGGGGAAGATTATATATATATAGTTTATAGAAAAATAACAAAAATATTTTCGAT	3380
Db	3055	TTCCGAGGGGGAAGATTATATATATATAGTTTATAGAAAAATAACAAAAATATTTTCGAT	3114
QY	3381	TAGTGGAAAAATTTGACTTTATAGAAAGAAAAATCTTTTCAAAAAATGCAATATTGAA	3440
Db	3115	TAGTGGAAAAATTTGACTTTATAGAAAGAAAAATCTTTTCAAAAAATGCAATATTGAA	3174
QY	3441	ACAGTTGAATGAAAAAGCAAAACCAAGTTTAAATTAACCAACCTTATTTATAGGATTTATAGG	3500
Db	3175	ACAGTTGAATGAAAAAGCAAAACCAAGTTTAAATTAACCAACCTTATTTATAGGATTTATAGG	3234
QY	3501	AAAGGAGAACAGCTGAATGAATATCCCTTTTGTGTAGAAACTGTCTTCAATGACGCTT	3560
Db	3235	AAAGGAGAACAGCTGAATGAATATCCCTTTTGTGTAGAAACTGTCTTCAATGACGCTT	3294
QY	3561	GTTAAAGTACAAATTTAAATATGTAATTCGCTCAATCACTACCAAGCCAGGTAAAG	3620
Db	3295	GTTAAAGTACAAATTTAAATATGTAATTCGCTCAATCACTACCAAGCCAGGTAAAG	3354
QY	3621	CAAGGGGCTATTTTTCGCTATCGCTCAAAATCAAGCATGATTCGCGGTGCTGTTGT	3680
Db	3355	CAAGGGGCTATTTTTCGCTATCGCTCAAAATCAAGCATGATTCGCGGTGCTGTTGT	3414
QY	3681	TCGTACTTCGAGGAGCGATTCAAGAAATCAGATACATTTACATTCGACACCCAA	3740
Db	3415	TCGTACTTCGAGGAGCGATTCAAGAAATCAGATACATTTACATTCGACACCCAA	3474
QY	3741	CGTTTATCGTTATGGAACGCTATGAGAGCAAAACCGTTTATACAGAAAGGACATTCGA	3800
Db	3475	CGTTTATCGTTATGGAACGCTATGAGAGCAAAACCGTTTATACAGAAAGGACATTCGA	3534
QY	3801	AAACAATTTAAGACAAATCAATACCTCTTTATGATTTGATTTTACAGCGCAAAAGA	3860
Db	3535	AAACAATTTAAGACAAATCAATACCTCTTTATGATTTGATTTTACAGCGCAAAAGA	3594
QY	3861	AACTATTTTACAGACCGGATATTTTAAACACCGCTATTTGATTTAGTCTTATCTAT	3920
Db	3595	AACTATTTTACAGACCGGATATTTTAAACACCGCTATTTGATTTAGTCTTATCTAT	3654
QY	3921	GATTATCAAAATCTGATAAAGGTTATCAAGCATATTTTGTGTTTGAAGCCGAGCTATGT	3980
Db	3655	GATTATCAAAATCTGATAAAGGTTATCAAGCATATTTTGTGTTTGAAGCCGAGCTATGT	3714
QY	3981	GACTTCAAAATCAGAAATTTAAATCTGCAAGACGCAAAATATTTTCGCAAAATATCCG	4040
Db	3715	GACTTCAAAATCAGAAATTTAAATCTGCAAGACGCAAAATATTTTCGCAAAATATCCG	3774
QY	4041	AGAATATTTTGGAAAGTCTTTGCCAGTTGATCTAACGCTGATATCATTTTGTGATGCTG	4100
Db	3775	AGAATATTTTGGAAAGTCTTTGCCAGTTGATCTAACGCTGATATCATTTTGTGATGCTG	3834
QY	4101	CATACCAAGACGGACATGAGATTTTTCACCTTAATTTACCGTTATTTCTTTCAAGA	4160
Db	3895	CATACCAAGACGGACATGAGATTTTTCACCTTAATTTACCGTTATTTCTTTCAAGA	3894

QY	4161	ATGCGAAGATTGGTCTTTTCAACCAACAGATAATAAGGGCTTTTACTCGTTCAGAGCTAAC	4220
Db	3895	ATGCGAAGATTGGTCTTTTCAACCAACAGATAATAAGGGCTTTTACTCGTTCAGAGCTAAC	3954
QY	4221	GTTTTTAAAGCGGTACAGAAAGCAAAAAACAAGTAGATGAACCCCTGGTTTAACTCTTATT	4280
Db	3955	GTTTTTAAAGCGGTACAGAAAGCAAAAAACAAGTAGATGAACCCCTGGTTTAACTCTTATT	4014
QY	4281	GCACGAACGAAATTTTTCAGGAGAAAGGGTTTAAATAGGGCTAATAACGTCATGTTTAC	4340
Db	4015	GCACGAACGAAATTTTTCAGGAGAAAGGGTTTAAATAGGGCTAATAACGTCATGTTTAC	4074
QY	4341	CCTCTCTTTAGCTACTTTTAGTTTCAGGGCTATTCAATCGAAACGTCGCAATATAATGTT	4400
Db	4075	CCTCTCTTTAGCTACTTTTAGTTTCAGGGCTATTCAATCGAAACGTCGCAATATAATGTT	4134
QY	4401	TGAGTTTAAATTCGATTAGATCAACCTTAGAGAGAAAGAAAGTAATCAAAATTTGTAG	4460
Db	4135	TGAGTTTAAATTCGATTAGATCAACCTTAGAGAGAAAGAAAGTAATCAAAATTTGTAG	4194
QY	4461	AAAGTGCCTATTTCAGAAAACTATCAAGGGCTAATAGGCAATACATTACCACTCTTTGCAA	4520
Db	4195	AAAGTGCCTATTTCAGAAAACTATCAAGGGCTAATAGGCAATACATTACCACTCTTTGCAA	4254
QY	4521	AGCTTGGGTATCAAGTGAATTTTAAACAGTAAAGATTTTATTTGTCGCTCAAGGGTGGTTAA	4580
Db	4255	AGCTTGGGTATCAAGTGAATTTTAAACAGTAAAGATTTTATTTGTCGCTCAAGGGTGGTTAA	4314
QY	4581	ATTCAAGAAAAAAGCAAGCAAGCTCAACGCTGTTTCTTTGTCAGAAATGGAAGAGATTT	4640
Db	4315	ATTCAAGAAAAAAGCAAGCAAGCTCAACGCTGTTTCTTTGTCAGAAATGGAAGAGATTT	4374
QY	4641	AATGCTTTATTTAGCGAAAAAAGCGATGTATACAAAGCTTATTTAGTGAAGCAACAAAA	4700
Db	4375	AATGCTTTATTTAGCGAAAAAAGCGATGTATACAAAGCTTATTTAGTGAAGCAACAAAA	4434
QY	4701	AGAGATTAGAAAGTCTAGGCAATTCCTGAACGGACATTAGATAAATTTGCTGAAGTACT	4760
Db	4435	AGAGATTAGAAAGTCTAGGCAATTCCTGAACGGACATTAGATAAATTTGCTGAAGTACT	4494
QY	4761	GAAAGCGCAATCAGGAAAAATTTCTTTAAGATTTAAACAGGAAAGAAATGGTGGCATTTCACT	4820
Db	4495	GAAAGCGCAATCAGGAAAAATTTCTTTAAGATTTAAACAGGAAAGAAATGGTGGCATTTCACT	4554
QY	4821	TGCTAGTGTAAATCATTTGTTGCTATCGATCATAAAGTAAAGAAAGAGAAAGAAAG	4880
Db	4555	TGCTAGTGTAAATCATTTGTTGCTATCGATCATAAAGTAAAGAAAGAGAAAGAAAG	4614
QY	4881	CTATATAAAGGGCGCTGACAAATTTCTTTTGACTTAGAGCATACATTTCAATCAAGAGACTTT	4940
Db	4615	CTATATAAAGGGCGCTGACAAATTTCTTTTGACTTAGAGCATACATTTCAATCAAGAGACTTT	4674
QY	4941	AAACAAGCTAGCAGAAAGCCCTTAAACCGGACACAACTCGATTTGTTTGTAGCTATGATAC	5000
Db	4675	AAACAAGCTAGCAGAAAGCCCTTAAACCGGACACAACTCGATTTGTTTGTAGCTATGATAC	4734
QY	5001	AGSGTGAATAAATAAACCCTGCTATGCCATTTACATTTATCTATGATACGTTTGTGTTT	5060
Db	4735	AGSGTGAATAAATAAACCCTGCTATGCCATTTACATTTATCTATGATACGTTTGTGTTT	4794
QY	5061	TTTCTTTGCTGTTTACGCAATGATTAGCAGAAATATACAGAGTAAGATTTTAAATTAATA	5120
Db	4795	TTTCTTTGCTGTTTACGCAATGATTAGCAGAAATATACAGAGTAAGATTTTAAATTAATA	4854
QY	5121	TTAGGGGGAAGAGGAGAGTAGCCGCAAACTTTTGTGTTGGCTTGGACTGAACCAAGTG	5180
Db	4855	TTAGGGGGAAGAGGAGAGTAGCCGCAAACTTTTGTGTTGGCTTGGACTGAACCAAGTG	4914
QY	5181	AGGAAAGGCTACTTAAACCGTCGAGGGCAGTGAGAGCGAAACGCACTTGAATTTTTTA	5240
Db	4915	AGGAAAGGCTACTTAAACCGTCGAGGGCAGTGAGAGCGAAACGCACTTGAATTTTTTA	4974
QY	5241	ATTTCTCTATCTTTTATAGTCAATAGAGTATACCTTATTTGTCCTATAAATTTTAGCAG	5300

Db 4975 ATTTCTATCTTTATAGGTCATTAGAGTATCTATTATTTGCTCTATAAACTATTTAGCAG 5034
Qy 5301 CATAATAGATTTTATGAATAGGTCATTAAAGTTGAGCATATTAGAGAGGAAAATCTTGG 5360
Db 5035 CATAATAGATTTTATGAATAGGTCATTAAAGTTGAGCATATTAGAGAGGAAAATCTTGG 5094
Qy 5361 AGAAATATTTGAAGAACCCGATTACATGGAATGAGTTAGTTCTTTGGTTACGTTGTTTT 5420
Db 5095 AGAAATATTTGAAGAACCCGATTACATGGAATGAGTTAGTTCTTTGGTTACGTTGTTTT 5154
Qy 5421 TAACTAAAGTACTGAAATTTTGAATTTTGGTGTGTGTCTTGTGTTAGTATTGCTA 5480
Db 5155 TAACTAAAGTACTGAAATTTTGAATTTTGGTGTGTGTCTTGTGTTAGTATTGCTA 5214
Qy 5481 GTCAAAAGTGATTAATA 5497
Db 5215 GTCAAAAGTGATTAATA 5231

RESULT 4
US-09-280-428A-11
; Sequence 11, Application US/09280428A
; Patent No. 6495738
; GENERAL INFORMATION:
; APPLICANT: Folkerts, Otto
; APPLICANT: Merlo, Donald J
; TITLE OF INVENTION: Modification of Fatty Acid Composition in Plants by
; FILE OF INVENTION: Expression of A Fungal Acyl-CoA Desaturase
; FILE REFERENCE: 50612
; CURRENT APPLICATION NUMBER: US/09/280,428A
; CURRENT FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: 60/079840
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 11
; LENGTH: 10323
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:pDAB1542
US-09-280-428A-11

Query Match 20.2%; Score 1111; DB 4; Length 10323;
Best Local Similarity 100.0%; Pred. No. 4.9e-234; Indels 0; Gaps 0;
Matches 1111; Conservative 0; Mismatches 0;

Qy 936 AAAAGAAAACGAAATGATACACCAATCAGTGCAGAAAAGATATTAATGGAGATAAGAC 995
Db 5286 AAAAGAAAACGAAATGATACACCAATCAGTGCAGAAAAGATATTAATGGAGATAAGAC 5345
Qy 996 GGTTCGTGTCGTCGCTGACTTGACCATATCATAAAATCGAAACGAAAGATGGCGG 1055
Db 5346 GGTTCGTGTCGTCGCTGACTTGACCATATCATAAAATCGAAACGAAAGATGGCGG 5405
Qy 1056 AAACGTAAGAAAGAGTTATGAAATAGACCTTAGAAGCAAACTTAAAGTGTGTGTATGT 1115
Db 5406 AAACGTAAGAAAGAGTTATGAAATAGACCTTAGAAGCAAACTTAAAGTGTGTGTATGT 5465
Qy 1116 GCAGTATCTTAAATTTTGTATTAATAGGAATGGAATTAATAGATGCTAAAAATTTGT 1175
Db 5466 GCAGTATCTTAAATTTTGTATTAATAGGAATGGAATTAATAGATGCTAAAAATTTGT 5525
Qy 1176 AATTAAGAGAGGTGATTACATGAACAAATAATAAATATCTCAAACTTTTAAACA 1235
Db 5526 AATTAAGAGAGGTGATTACATGAACAAATAATAAATATCTCAAACTTTTAAACA 5585
Qy 1236 GTGAAAAAGTACTCAACCAAAATTAATAAATTAATTAAGAAACCGATACCGTTT 1295
Db 5586 GTGAAAAAGTACTCAACCAAAATTAATAAATTAATTAAGAAACCGATACCGTTT 5645
Qy 1296 ACGAATTTGGAACAGGTAAAGGCGCATTTACAGCAGAACTGGCTAAAAATAGTAAACAGG 1355

Db 5646 ACGAATTTGGAACAGGTAAAGGCGCATTTAACGAGAACTGGCTAAAAATAGTAAACAGG 5705
Qy 1356 TAAAGTCTATTGAATTAAGACAGTCTATCTTATTTCACTTATCGTCAGAAAAATTTAAACCTGA 1415
Db 5706 TAAAGTCTATTGAATTAAGACAGTCTATCTTATTTCACTTATCGTCAGAAAAATTTAAACCTGA 5765
Qy 1416 ATACTCGTGTCACTTTAATCCCAAGATATTTACAGATTTCATTTCCCTTCAACAAACAGA 1475
Db 5766 ATACTCGTGTCACTTTAATCCCAAGATATTTACAGATTTCATTTCCCTTCAACAAACAGA 5825
Qy 1476 GGTATTAATTTGTTGGAGTATTCCTTACCAATTTTAAAGCACAACAATTTATTAAGAAAGTGG 1535
Db 5826 GGTATTAATTTGTTGGAGTATTCCTTACCAATTTTAAAGCACAACAATTTATTAAGAAAGTGG 5885
Qy 1536 TTTTGTAAAGCCATGCGCTCTGACATCTATCTGATTTGTTGAAGAGGATTTCTACAAGCGTA 1595
Db 5886 TTTTGTAAAGCCATGCGCTCTGACATCTATCTGATTTGTTGAAGAGGATTTCTACAAGCGTA 5945
Qy 1596 CTTTGGATATTACCGAACAACCTAGGTTGCTCTTGGACACTCAAGTCTCGATTTCAGCAAT 1655
Db 5946 CTTTGGATATTACCGAACAACCTAGGTTGCTCTTGGACACTCAAGTCTCGATTTCAGCAAT 6005
Qy 1656 TGCTTAAGCTGCCAGCGGAATGCTTTTCACTCTAAACCAAAAGTAAACAGTCTCTTAATAA 1715
Db 6006 TGCTTAAGCTGCCAGCGGAATGCTTTTCACTCTAAACCAAAAGTAAACAGTCTCTTAATAA 6065
Qy 1716 AACTTACCCGCAATACACAGATGTTCCAGATAAATTTGGAAGCTATATACGTAATTTG 1775
Db 6066 AACTTACCCGCAATACACAGATGTTCCAGATAAATTTGGAAGCTATATACGTAATTTG 6125
Qy 1776 TTTCAAAATGGTCAATCGAGAATATGTCACCTGTTTACTTAAATAACAGTTTCATCAAG 1835
Db 6126 TTTCAAAATGGTCAATCGAGAATATGTCACCTGTTTACTTAAATAACAGTTTCATCAAG 6185
Qy 1836 CAATGAAACACGCCAAAGTAAACAAATTTAAGTACCGTTACTTTAGAGCAAGTATTTGCTA 1895
Db 6186 CAATGAAACACGCCAAAGTAAACAAATTTAAGTACCGTTACTTTAGAGCAAGTATTTGCTA 6245
Qy 1896 TTTTAAATAGTATCTATTTTAAACCGAGGAATTAATCTATGAGTCGCTTTTGTAAA 1955
Db 6246 TTTTAAATAGTATCTATTTTAAACCGAGGAATTAATCTATGAGTCGCTTTTGTAAA 6305
Qy 1956 TTTGAAAGTTACACGTTACTTAAAGGGAATTAGATAAAATTTATTTAGGTATACTACTGACA 2015
Db 6306 TTTGAAAGTTACACGTTACTTAAAGGGAATTAGATAAAATTTATTTAGGTATACTACTGACA 6365
Qy 2016 GCTTCCAAAGAGCTAAAGAGGTCCCTAGCGC 2046
Db 6366 GCTTCCAAAGAGCTAAAGAGGTCCCTAGCGC 6396

RESULT 5
US-09-056-075-1/c
; Sequence 1, Application US/09056075
; Patent No. 5955368
; GENERAL INFORMATION:
; APPLICANT: Johnson, Eric A.
; APPLICANT: Bradshaw, Marite
; APPLICANT: Rood, Julian
; TITLE OF INVENTION: Expression System for Clostridium
; TITLE OF INVENTION: Species
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

Db 462 AACACTAGGTTGCTCTTGACCACTCAAGTCTCGAATTCAGCAATTCGTTAAGTGCAGC 521
QY 1672 GGAATGCTTTTCATCCCTAAACCAAGTAPACAGTGTCTTAATAAATCTTACCGCCATAC 1731
Db 522 GGAATGCTTTTCATCCCTAAACCAAGTAPACAGTGTCTTAATAAATCTTACCGCCATAC 581
QY 1732 CACAGATGTTCCAGATAAATATTGGAAGCTATATAGCTACTTTGTTTCAAAATGGGTCAA 1791
Db 582 CACAGATGTTCCAGATAAATATTGGAAGCTATATAGCTACTTTGTTTCAAAATGGGTCAA 641
QY 1792 TCGAGATATCGTCAAGTGTCTTACTAATAAATCAGTTTCATCAAGCAATGAACACGCCAA 1851
Db 642 TCGAGATATCGTCAAGTGTCTTACTAATAAATCAGTTTCATCAAGCAATGAACACGCCAA 701
QY 1852 AGTAACAATTAAGTACCGTCTTACTATGACCAAGTATTGCTCTATTTTAAATAGTTATCT 1911
Db 702 AGTAACAATTAAGTACCGTCTTACTATGACCAAGTATTGCTCTATTTTAAATAGTTATCT 1911
QY 1912 ATTATTTAAGGGAGGAATAA 1933
Db 762 ATTATTTAAGGGAGGAATAA 783

RESULT 7
US-08-743-637B-193
; Sequence 193, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: QUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,637B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,840
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850886.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 193:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-743-637B-193

Query Match 13.3%; Score 731.6; DB 2; Length 738;
Best Local Similarity 99.5%; Pred. No. 3.1e-151;
Matches 734; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1196 ATGACCAAAATATATAAATATCTCAAAACCTTTTAAAGAGTGAAGAGTACTCAACAA 1255
Db 1 ATGACCAAAATATATAAATATCTCAAAACCTTTTAAAGAGTGAAGAGTACTCAACAA 60
QY 1256 ATAATAAAACAATTTGAATTTTAAAGAAACCGATACCGTTTACGAAATTTGGAACAGGTAAA 1315
Db 61 ATAATAAAACAATTTGAATTTTAAAGAAACCGATACCGTTTACGAAATTTGGAACAGGTAAA 120
QY 1316 GGGCATTTAAGCAAGAACTCGCTTAAATTAAGTAAACAGGTAAACGTCTATTGAATAGAC 1375
Db 121 GGGCATTTAAGCAAGAACTCGCTTAAATTAAGTAAACAGGTAAACGTCTATTGAATAGAC 180
QY 1376 AGTCATCTATTCAACTTATCGTCAGAAAAATTTAAATTCGAATCTCGTGTCACTTTAAT 1435
Db 181 AGTCATCTATTCAACTTATCGTCAGAAAAATTTAAATTCGAATCTCGTGTCACTTTAAT 240
QY 1436 CACCAAGATATTCTACAGTTTCAATTCCTTAAACAGAGGTATATAAATTTGTTGGAGT 1495
Db 241 CACCAAGATATTCTACAGTTTCAATTCCTTAAACAGAGGTATATAAATTTGTTGGAGT 300
QY 1496 ATTCCTTACCATTAAAGCACACAAATTTATTAAGAGTGGTTTTTGAAGCGATCGCTCT 1555
Db 301 ATTCCTTACCATTAAAGCACACAAATTTATTAAGAGTGGTTTTTGAAGCGATCGCTCT 360
QY 1556 GACATCTATCTGATTGTTGAAGAGGATTCTACAAGCGTACTCTGGATATTCAACGAACA 1615
Db 361 GACATCTATCTGATTGTTGAAGAGGATTCTACAAGCGTACTCTGGATATTCAACGAACA 420
QY 1616 CTAGGGTTCTCTGCACACTCAAGTCTCGATTGAGCAATTCCTTAAGTCCGACGGAA 1675
Db 421 CTAGGGTTCTCTGCACACTCAAGTCTCGATTGAGCAATTCCTTAAGTCCGACGGAA 480
QY 1676 TCGTTTCTATCTTAAACCAAGTAAACAGTGTCTTATATAAATTTACCGCATACCA 1735
Db 481 TCGTTTCTATCTTAAACCAAGTAAACAGTGTCTTATATAAATTTACCGCATACCA 540
QY 1736 GATGTTCCAGATAAATATTGGAAGCTATATAGTACTTTGTTTCAAAATGGTCAATCGA 1795
Db 541 GATGTTCCAGATAAATATTGGAAGCTATATAGTACTTTGTTTCAAAATGGTCAATCGA 600
QY 1796 GAATATCGTCAACTGTTTACTTAAATAATCAGTTTCAATCAAGCAATGAACACGCCAAAGTA 1855
Db 601 GAATATCGTCAACTGTTTACTTAAATAATCAGTTTCAATCAAGCAATGAACACGCCAAAGTA 660
QY 1856 AACAAATTTAAGTACCGTTTACTTATGAGCAAGTATGCTATTATTTAATAGTTATCTATA 1915
Db 661 AACAAATTTAAGTACCGTTTACTTATGAGCAAGTATGCTATTATTTAATAGTTATCTATA 720
QY 1916 TTTRACGGGAGGAATAA 1933
Db 721 TTTRACGGGAGGAATAA 738

RESULT 8
US-09-134-000C-3296
; Sequence 3296, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3296

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; LENGTH: 1167
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3296

Query Match
Best Local Similarity 55.0%; Score 273.2; DB 4; Length 1167;
Matches 630; Conservative 0; Mismatches 498; Indels 18; Gaps 4;

QY 3517 ATGAATATCCCTTTTGGTTGTAAGAACTGCTTCAATGACGCTTGTGTTAAAGTACAAATTT 3576
D 13 ATGAAGTTCTGAGGTTATTTCTAGTTATTTTAAAGATGCGCATTCGTGAATACAAATAT 72
QY 3577 AAAAATAGTAAATTTCCGCTCAATCACTACCAAGCCAGTAAAGCAAGGGGCTATTTT 3636
D 73 TTAACACAAATTTAAACCAATCGCTATTAAGCTGAAGGAAAGAGTGCTATTTT 132
QY 3637 GCGTATCGCTCAAAATCAAGCATGATTTGGCGGTGCTGGTGTGTTCTGACTTCCGAGAA 3696
D 133 GGGTTAGATCAAGGAGTTAATGACGGAATCTCGTGAATCGTTCTTACTTCTCAAGAA 192
QY 3697 CGGATTCAGAAATCAAGATACATTTACATTTGGACACCCACCGATTTCGTATGGA 3756
D 193 GCGTTAGCTGAATGAAATGAAATTTACTCATTTGGACCCCTAATGTTTATGTTATGTT 252
QY 3757 ACGTATGACAGCAAAACCGTTTCATACAGAAAGGACATTTCTGAAACAAATTTAAGCAA 3816
D 253 GCATATGCTGATGATAATAGAACTATTGTTAAAGGCCACACGAAAGAACTTGCACAA 312
QY 3817 ATCAATACCTTTTATGATTTTGAATTTCAACGCGCAAGAAAGAACTTTTCAGCAAGC 3876
D 313 ATCAATACCTTTTGAATTCGATTTTGA---TCGCTCACTAGTGAAATATTAGATTCTCAA 369
QY 3877 GATATTTTAAACACCGCTATTGATTTAGTTTATGCTTACTATGATTTCAAACTCTGAT 3936
D 370 ATGATTTCTGATGCTGCAATGATCTGGAACGTATGCCAAGCTAATTTTAGAACTCCA 429
QY 3937 AAAGTTATCAAGCATATTTTGGTTTGTAGAAAGCGGAGTCTATGCTGACTTCAAAATCGAA 3996
D 430 GGGGATTTCAAGCGTATTTCAITCTTTGAAATGCGCTGGTACATTTCTTCAAAAATPAAT 489
QY 3997 TTTAAATCTGTCAAGACGCAAAATATTTTCGCAAAATATCCGAGAAATTTTGGAAAG 4056
D 450 TATCAATCAATCGAAGTGGCCAGAGAGTATCTGAAATTTAAGAAAGCAATTTGCTGAA 549
QY 4057 TCTTTGCG---CAGTTGATCTAACGTTAATCATTTTGGTATTTGCTGCAATCCAAAGACG 4113
D 550 GTATTTGCCCTTCGGTGGATTTGGGGTGGCAACCAATTTTGGTATTTGACGCTATTTCTAGAAC 609
QY 4114 GCAATGTAGAAATTTTGTGCTCTTAATTCAGCTTATTTTCAAGATGCGAAGATTTG 4173
D 610 GCAATGTAGTCTATTAATCTCCAGCTGACATGATATGCAACAACTAATCCAGTGG 659
QY 4174 TCTTTCAACAAACAGATAATTAAGGGCTTTTACTCGTTCAAGTCTAACCGGTTTAAAGCGGT 4233
D 670 TCCATGAAATTTGAGCCAAAGAAACACATAAAACCGAATCTTAATGTT-----GTT 723
QY 4234 ACAGNAGGCAAAACAGATGATGACCTGTTTAAATCTCTTATTTGACGAAACGAAA 4293
D 724 GCTGTAAAGATGAATCAGATTAAGAGCAGTGGGTTAAAGTTTAAATGATAATCCGCAA 783
QY 4294 TTTTCAGGAGAAAGGGTTTAAATAGGGGTAATTAACGTCATGTTTACCTCTCTTTAGCC 4353
D 784 GTCGTCGCTACTAAAGGAAACTAGGACGAAACAATGTAATTTTACTTTATCTTTGCT 843
QY 4354 TACTTTAGTTCAGGCTTATCAATCGAAACGTGCGAATATATATATGTTTGGTTTAAATAT 4413
D 844 TACTATGCGCTCAAAAATTTGAACAAGACCGCTGTTTGTATGATATGGATGATTTCAACAGT 903
QY 4414 CGATTAGATCAACCTTTAGAAAGAAAGAAAGTAAATCAAAATTTGTAGAAAGTGCCTATTCA 4473
D 904 TCTTTGAATATCTCTATCAGTTTCAGAAATAAGAGAAATTTGTAGAGTGTCTTACTCA 963

RESULT 9
US-09-134-000C-3315
; Sequence 3315, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: LYNN Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3315
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3315

Query Match 4.5%; Score 247.2; DB 4; Length 696;
Best Local Similarity 93.5%; Pred. No. 4.6e-45;
Matches 258; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 663 ATCGATACGATTTTGAAGTGGCAACAGATATAAAAGACAGTTTAAAAATTTGTTGTAAC 722
D 230 ATCGATACGATTTTGAAGTGGCAACAGATATAAAAGACAGTTTAAAAATTTGTTGTAAC 289
QY 723 TTTTAAACAAAGCAAAATCAATCATTTGCGCAACAGATAGCGACAGAGAGCGGAAACAA 782
D 290 TTTCTCAAAAGGCAAAATCAATTTATTGTCGAACAGATAGCGACAGAGAGCGTGAATA 349
QY 783 TTGCGCTGGTCGATCATTTCAAAAGCAAAATGCTTTTCTAAAGATAAAACGATATAAGAC 842
D 350 TCGCTTGGTCGATTAATCCATTAAGCAAAATGCTTTTCTAAAGATAAAACGATATAAGAT 409
QY 843 TATGATCAATAGTTTAGAAAAAGATGTATCCGTCGCGTTTCAAAATTTGCAACCG 902
D 410 TATGATCAATAGTTTAGAAAAAGATGTATCCGTCGCGTTTCAAAATTTGCAACCG 469
QY 903 GAATGAATTAATCTCCCTTTTATCAAGAGCGCAA 938
D 470 GAATGAATTAATCTCCCTTTTATCAAGAGCGCAA 505

RESULT 10
US-08-992-334-1/c
; Sequence 1, Application US/08992334
; Patent No. 5919678
; GENERAL INFORMATION:
; APPLICANT: Gruss, Alexandra
; APPLICANT: Maguin, Emmanuelle
; TITLE OF INVENTION: METHODS FOR USING A TEMPERATURE-SENSITIVE
; TITLE OF INVENTION: PLASMID
; NUMBER OF SEQUENCES: 3
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Christie Parker & Hale, LLP
;; STREET: 350 West Colorado Boulevard, Suite 500
;; CITY: Pasadena
;; STATE: California
;; COUNTRY: United States
;; ZIP: 91105

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/992,334

;; FILING DATE: 17-DEC-1997

;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/302,752

;; FILING DATE: 24-DEC-1994

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: PCT/FR93/00248

;; FILING DATE: 12-MAR-1993

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: FR 992/03034

;; FILING DATE: 13-MAR-1992

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Prout, D. Bruce

;; REGISTRATION NUMBER: 20958

;; REFERENCE/DOCKET NUMBER: C93:31779

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (626) 795-9900

;; TELEFAX: (626) 577-8800

;; INFORMATION FOR SEQ ID NO: 1:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 3792 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: both

;; TOPOLOGY: circular

;; MOLECULE TYPE: DNA (genomic)

;; HYPOTHETICAL: NO

;; ANTI-SENSE: YES

;; IMMEDIATE SOURCE:

;; CLONE: pg+host4

;; US-08-992-334-1

Query Match 4.4%; Score 244.2; DB 2; Length 3792;

Best Local Similarity 58.0%; Pred. No. 3.6e-44; Indels 0; Gaps 0;
Matches 432; Conservative 0; Mismatches 313;

QY 1176 AATTAGAAGGAGTGAATTAATGAACAAATAATAAATAATCTCAAACTTTTAAACGA 1235

DB 815 AATTAGAAGGAGTGAATTAATGAACAAATAATAAATAATCTCAAACTTTTAAACGA 1235

QY 1236 GTGAAAAGTACTCAACCAATAATAAACAATTGAATTTAAAGAAACCGATACCGTTT 1295

DB 755 CAAAACATAATATAGATAAATAATGAACAAATAATAAAGATTAAATGAACATGATAATCT 696

QY 1296 ACGAATTTGAACAGGTAAGGAGGATTTAAGCAGCAACTGGCTAAATAAGTAAACAGG 1355

DB 695 TTGAATCGCTCAGGAAGGAGGCAATTTACCTTGNATTAGTAAGAGGAGTGAATTCG 636

QY 1356 TAACGCTATTGAATTAAGACAGTCACTATCTCAACTTATCGTCAGAAAAATTAACACTGA 1415

DB 635 TAACGCTATTGAATTAAGACAGTCACTATCTCAACTTATCGTCAGAAAAATTAACACTGA 1415

QY 1416 ATACTCGTGTCACCTTTAAATTCACCAAGATATCTCAAGTTTCAATTCCTCCCTAACCAACAGA 1475

DB 575 ACGATAATTTCCAAAGTTTAAACAAGGATATATTGCGAGTTTAAATTTCTTAAACCAAT 516

QY 1476 GGTATAAAATTTGGGAGTATCTCTTACCACTTTAAGCAGCACAATAATTATTAATAAAAGTGG 1535

DB 515 CCTATAAAATATATGGTAATATACCTTTAATACATAAGTACGGATATAATACGCAAAATTC 456

QY 1536 TTTTGAAGCCATCGCTGACATCTATCTGATTTGAAGAAGGATTTTACAAGCTA 1595

DB 455 TTTTGTAGTAGTATAGCTAATGAGATTTTATTAATCGTGAATACGGGTTTCTAAAGAT 396

QY 1596 CTTGCGATTTACCGAACACTAGGGTTGCTCTTCCACACTCAAGTCTCGATTGAGCAAT 1655

DB 395 TATTAAATACAAACGCTCATTTGGCAATTTTAAATGGCAGAGTTGATATTTCTATAT 336

QY 1656 TGCCTTAAGCTGCCAGCGGAATGCTTTTCATCTCTAAACCAAAAGTAAACAGTGTCTTAAATA 1715

DB 335 TAAAGTATGGTTCCAGAGAAATATTTTCATCTCTAAACCTAAAGTGAATAGCTCACATCA 276

QY 1716 AACTTACCCGCCATACACAGATGTTCCAGATAAATATTGGAAGCTATATAGTACTTTG 1775

DB 275 GATTAAAGTAGAAAAAATCAAGAATATCACAAAAAGATAAATAATTTATTTTCG 216

QY 1776 TTTCAAAATGGTCAATCGAGAATATCTCAACTGTTTACTAAAAATCAGTTTTCATCAAG 1835

DB 215 TTATGAATGGTTTAAACAAAGATACAGAAATATTTTACAAAAATCAATTTAACAT 156

QY 1836 CAATGAAACACGCCAAAGTAAACAATTTAAGTACCGTTTACTTATGAGCAAGTATTGTCTA 1895

DB 155 CCTTAAACATGCGAGGAATTCACGATTTTAAACAATATTAGCTTTGAACAATTTCTTATCTC 96

QY 1896 TTTTAAATAGTTATCTATTATTAA 1920

DB 95 TTTTCAATAGCTATAAATTTTAA 71

RESULT 11

US-08-302-752-1/c

; Sequence 1, Application US/08302752

; Patent No. 6025190

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: THERMOSENSIBLE PLASMID

; NUMBER OF SEQUENCES: 3

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/302,752

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 9203034

; FILING DATE: 13-MAR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO FR/93/00248

; FILING DATE: 12-MAR-1993

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3792 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-302-752-1

Query Match

Best Local Similarity 58.0%; Pred. No. 3.6e-44;

Matches 432; Conservative 0; Mismatches 313; Indels 0; Gaps 0;

QY 1176 AATTAGAAGGAGTGAATTAATGAACAAATAATAAATAATCTCAAACTTTTAAACGA 1235

DB 815 AATTAGAAGGAGTGAATTAATGAACAAATAATAAATAATCTCAAACTTTTAAACGA 1235

QY 1236 GTGAAAAGTACTCAACCAATAATAAACAATTGAATTTAAAGAAACCGATACCGTTT 1295

DB 755 CAAAACATAATATAGATAAATAATGAACAAATAATAAAGATTAAATGAACATGATAATCT 696

QY 1296 ACAGAAATTTGGAACAGGTAAGGCGATTTAAGACGAACTGGCTAAATAAGTAACAGG 1355
DB 695 TTGAATCGGCTCAGAAAGGCGCATTTTACCCTGTAATAGTAAGAGGTGTAATTCG 636
QY 1356 TAACGCTTATTGAATGACAGAGTCACTTAATCACTTATCGTCAGAAAAATTAACCTGA 1415
DB 635 TAACGCTTATTGAATGACAGAGTCACTTAATCACTTATCGTCAGAAAAATTAACCTGA 576
QY 1416 ATACTCGTGCACATTTAATTCACCAAGATTTCTACAGTTTCAATTCCTTAACAGAGCA 1475
DB 575 ACAGATAATTTCCAGATTTTAAACCAAGGATATATTGCGAGTTTAAATTTCCCTAAACCAAT 516
QY 1476 GGTATAAAATTTGGGAGTATTCCTTACCAATTTAAGCACACAAATTTAATAAAAGTGG 1535
DB 515 CCTATAAATATATGGTAATATACCTTATACATAAGTACGATATATACGCAAAATG 456
QY 1536 TTTTGAAGCGATCGCTGCACATCTATCTGATTTGAAGAGGATTTACAGCGTA 1595
DB 455 TTTTGTATAGTATAGCTAATCAGATTTATTTAATCGTGAATACGGGTTTGCCTAAAGAT 396
QY 1596 CTTGGATATTACCGAACACTAGGTTGCTCTTGCACACTCAAGTCTCGATTCAGCAAT 1655
DB 395 TATTAAATACAAACGCTCATTTGCAATTTTAAATGCGAGAGTTGATATTTCTATAT 336
QY 1656 TCGTTAAGCTCGGAGGAAATGCTTTTCATCTTAACCAAGGATTAACAGAGTCTTAATAA 1715
DB 335 TAAGTATGTTTCCAGAGATATTTTTCATCTTAAACCTTAAAGTGAATAGCTCACTATCA 276
QY 1716 AACTTACCCTGCATACACAGATGTTCCAGATAATATTTGAAGCTATATACGTTTTCG 1775
DB 275 GATTAAAGTAGAAAAATCAAGATATCACAAAGATTAACAAAGATTAATTTTCG 216
QY 1776 TTTCAAAATGGTCAATCGAGATATCGTCACTGTTTACTTAAAAATCAGTTTCAATCAAG 1835
DB 215 TTATGAATGGTTTAAACAAAGATACAGAAATATTTTACAAAAATCAATTTAACAAT 156
QY 1836 CAATGAACAGCCAAAGTAACAAATTTAAGTACGGTTACTTATGACAGATTTGCTA 1895
DB 155 CTTTAAACATGCGAGGATGACGATTTAAACAAATATAGCTTTGAACAAATTTCTATCTC 96
QY 1896 TTTTAAATAGTATCTATTTAA 1920
DB 95 TTTTCAATAGCTATAATTTAA 71

RESULT 12

US-08-992-334-2/c
; Sequence 2, Application US/08992334
; Patent No. 5919678
; GENERAL INFORMATION:
; APPLICANT: Gruss, Alexandra
; TITLE OF INVENTION: METHODS FOR USING A TEMPERATURE-SENSITIVE
; TITLE OF INVENTION: METHODS FOR USING A TEMPERATURE-SENSITIVE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christie Parker & Hale, LLP
; STREET: 350 West Colorado Boulevard, Suite 500
; CITY: Pasadena
; STATE: California
; COUNTRY: United States
; ZIP: 91105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/992.334
; FILING DATE: 17-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/302,752

FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00248
FILING DATE: 12-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 992/03034
FILING DATE: 13-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Prout, D. Bruce
REGISTRATION NUMBER: 20958
REFERENCE/DOCKET NUMBER: C93:31779
TELEPHONE: (626) 795-9900
TELEFAX: (626) 577-8800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5234 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
US-08-992-334-2
Query Match 4.4%; Score 244.2; DB 2; Length 5234;
Best Local Similarity 58.0%; Pred. No. 4e-44; Mismatches 313; Indels 0; Gaps 0;
Matches 432; Conservative 0;
QY 1176 AATTAAGAGGAGTGTATACATGAAACAAAAATATAAAATATTTCTCAAACTTTTAAACGA 1235
DB 2257 AATTAAGAGGTTTATTAATGAACGAGAAAAATATAAAACACAGTCAAACTTTTACTT 2198
QY 1236 GTGAAAAAGTACTCAACCAATATAAACAATTAATGCAATTTAAAGAACCGATACCGTTT 1295
DB 2197 CAAAACATAATATAGATAAAATTAATGCAAAATATAAGATTAATGAACATGATATATCT 2138
QY 1296 ACGAAATGGAACAGGTAAAGGGCATTTAAACGACAAAACCTGGCTAAAAATAAGTAAACAGG 1355
DB 2137 TTGAATCGGCTCAGAAAAAGGCCATTTTACCTTGAATTAAGAGAGGTGTAATTTTCG 2078
QY 1356 TAACGTCTATTGAATAGACAGTCACTTATCACTTATCGTCAGAAAAATTAACACTGA 1415
DB 2077 TAACGTCTATTGAATAGACAGTCACTTATCACTTATCGTCAGAAAAATTAACACTGA 2018
QY 1416 ATACTCGTGTCACTTTAATTCACCAAGATATTTACAGTTTCAATTCCTCAACAAACAGA 1475
DB 2017 ACGATAATTTCCAGTTTAAACAGGATATATTCGAGTTTAAATTTCTTAACCAAT 1958
QY 1476 GGTATAAAATTTGGGAGTATTCCTTACCATTAAAGCACACAAATTAATAAAAGTGG 1535
DB 1957 CCTATAAAATATATGTTAATATACCTTATAACATAAGTACGGATATAATACGCAAAATG 1898
QY 1536 TTTTGAAGCCATCGCTGACATCTATCTGATTTGTTGAAGAGGATTTCTACAGCGTA 1595
DB 1897 TTTTGAATAGTATAGCTAATGAGATTTTAACTGTCGATACCGGTTTGTCTAAAGAT 1838
QY 1596 CTTTGGATATTCACCGAACACTAGGTTTGTCTTTCACACTCAAGTCTCGATTCAGCAAT 1655
DB 1837 TATTAAATACAAACCGCTCATTTGGCATTTACTTTAATGCGCAGAGTTGATATTTCTATAT 1778
QY 1656 TCGTTAAGCTGCGAGGAGTCTTTTCATCTTAAACCAAGGATTAACAGTGTCTTAATAA 1715
DB 1777 TAAGTATGTTTCCAGAGATATTTTTCATCTTAAACCTTAAAGTGAATAGCTCACTATCA 1718
QY 1716 AACTTACCGCCATACCCAGATGTTCCAGATAAATATTTGAAGCTATATACGTAATTTG 1775
DB 1717 GATTAAAGTAGAAAAATCAAGATATCACACAAAGATATAAACAAGTATAATTTTCG 1658
QY 1776 TTTTCAAAATGGTCAATCGAGATATCGTCACTGTTTACTTAAAAATCAGTTTCACTAAG 1835
DB 1657 TTAGAAATGGGTTAAACAGAAATATTTTACAAAAATCAATTTTAACTT 1598
QY 1836 CAATGAACACGCGCAAGTAAACAAATTTAAGTACCGTTACTTATGAGCAAGTATTGCTA 1895

Db 1597 CCTTAAACATGCGAGGATTCAGCATTTAAACAATATTAGCTTTGAACAATTCCTTATCTC 1538

Qy 1896 TTTTAAATAGTTATCTATTATTAA 1920

Db 1537 TTTTCAATAGCTATAAATTATTAA 1513

RESULT 13

US-08-302-752-2/c

; Sequence 2, Application US/09302752

; Patent No. 6025190

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: THERMOSENSIBLE PLASMID

; NUMBER OF SEQUENCES: 3

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/302,752

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 9203034

; FILING DATE: 13-MAR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO FR/93/00248

; FILING DATE: 12-MAR-1993

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5234 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-302-752-2

Query Match 4.4%; Score 244.2; DB 3; Length 5234;

Best Local Similarity 58.0%; Pred. No. 4e-44;

Mismatches 432; Conservative 0; Mismatches 313; Indels 0; Gaps 0;

Qy 1176 AATTAGAAGGATGATCATGACGACAAATATATAATTTCTCAAACTTTTAAACGA 1235

Db 2257 AATTAGAAGGATGATCATGACGACAAATATATAATTTCTCAAACTTTTAACTT 2198

Qy 1236 GTGAAAAGTACTCAACCAATATAAACAATTTGAATTTAAAGAAACCGATACCGTTT 1295

Db 2197 CAAACATAATATAGATAAATAATATGCAATATATAGATTAAATGACATGATATCT 2138

Qy 1296 ACGAAATTGGAACAGGTAAGGCAATTAACGACGAACTGGCTAAATAAGTAAACAGG 1355

Db 2137 TTGAAATCGGCTCAGGAAAGGCAATTTACCCCTTGAATTTAGTAAAGAGGTTGTAATTCG 2078

Qy 1356 TAAGCTCTATTGAATTAGACAGCATCTATTCACTTATCGTCAGAAAATTTAAACTGA 1415

Db 2077 TAAGCTCTATTGAATTAGACCAATTAATATGCAAACTACAGAAAATAAATCTTTGATC 2018

Qy 1416 ATACTCGTGTCACTTTAAATTCACCAAGATATTTCAAGTTTCAATTTCCCTTAAACAAACAGA 1475

Db 2017 ACGATAATTTCCAGTTTAAACAAGGATATTTGCAAGTTTAAATTTCCCTTAAACCAAT 1958

Qy 1476 GGTAATAAATTTGGGAGATTTCCCTTACCATTTAAGCACACAAATTTAAATAAGTGG 1535

Db 1957 CCTATAAATAATATGGTAATATACCTTTATACATAAGTAGCGGATATAATACGCAAAATTG 1898

Qy 1536 TTTTGAAGCCATCGCTCGACATCTATCTGATTTGTTGAAGAGGATTTCAACGCTA 1595

Db 1897 TTTTGTATAGTATAGCTAAATGAGATTTATTTATCTGGAATACGGGTTGCTAAAGAT 1838

Qy 1596 CCTTGGATATTCACCGAACACTAGGTTGCTCTTTGACACTCAAGTCTCAATTCAGCAAT 1655

Db 1837 TATTAAATACAAAACGCTCATTTGGCATTACTTTTAAATGCGAGAGTTGATATTTCTATAT 1778

Qy 1656 TGTCTTAAGCTGCCAGCGGAATGCTTTTCATCTCTAAACAAAAGTAAACAGTGTCTTAAATA 1715

Db 1777 TAAAGTATGGTTCCAAAGAGATATTTTTCATCTCTAAACCTTAAAGTGAATAGCTCACTTATCA 1718

Qy 1716 AACTTACCCGCATACACAGATGTTCCAGATAAATATTGGAAGCTATATAGTACTACTTTG 1775

Db 1717 GATTAAGTAGAAAAAATCAAGATATCACAAAGATAAACAAGATTAATATTATTCG 1658

Qy 1776 TTTCAAAATGGTCAATCGAGAATATCGTCAACTGTTTACTTAAATAATCAGTTTCAATCAAG 1835

Db 1657 TTATGAAATGGTTTAAACAAGATATACAGAAAAATATTACAAAAAATCAATTTAAACAAT 1598

Qy 1836 CAATGAAACACGCCAAAGTAAACAATTTAAGTACCGTTTACTTATGAGCAAGTATTGTCTA 1895

Db 1597 CCTTAAACATGCGAGGAATTTGACGATTTTAAACAATTTAGCTTTGAACAATTTCTTATCTC 1538

Qy 1896 TTTTAAATAGTTATCTATTATTAA 1920

Db 1537 TTTTCAATAGCTATAAATTATTAA 1513

RESULT 14

US-09-329-920-1/c

; Sequence 1, Application US/09329920

; Patent No. 6326206

; GENERAL INFORMATION:

; APPLICANT: Bjornvad, Mads Eskelund

; APPLICANT: Rasmussen, Michael Dolberg

; APPLICANT: Jorgensen, Per Lina

; APPLICANT: Borchert, Torben Vedel

; APPLICANT: Ehrlich, Dr. Stanislas Dusko

; TITLE OF INVENTION: In Vivo Recombination

; FILE REFERENCE: 4833-204-US

; CURRENT APPLICATION NUMBER: US/09/329,920

; CURRENT FILING DATE: 1999-08-10

; PRIOR APPLICATION NUMBER: 60/050,590

; PRIOR FILING DATE: 1997-06-24

; PRIOR APPLICATION NUMBER: 1471/96

; PRIOR FILING DATE: 1996-12-20

; PRIOR APPLICATION NUMBER: 0592/97

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 0935/97

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 5313

; TYPE: DNA

; ORGANISM: Homologous

US-09-329-920-1

Query Match 4.4%; Score 244.2; DB 4; Length 5313;

Best Local Similarity 58.0%; Pred. No. 4e-44;

Mismatches 432; Conservative 0; Mismatches 313; Indels 0; Gaps 0;

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Db 4340 AATTAGAAGGATGATTAATGACGAGAAAAATATAAACAAGTCAAACTTTTACTT 4281

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Db 4280 CAAACATAATATAGATAAATAATATGCAATAATATAGTTAAATGACATGATATCT 4221

Qy 1296 ACGAAATTGGAACAGGTAAGGCAATTTAAGCAAGAACTGGCTAAATAAGTAAACAGG 1355

Db 4220 TTGAAATCGGCTCAGGAAAGGCCATTTTACCCCTTGAATTTAGTAAAGAGGTTGTAATTCG 4161

Qy 1356 TAACTGTCTATTGAATTAGACAGTCTATCTATTCACTTATCTGTCAGAAAAATTAACGTA 1415

Db 4160 TAACTGCCATTGAATAGACCAATTAATTTGCAAACTACAGAAAAATTAACCTGTTGATC 4101

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QY 1416 ATACTCGTGCACCTTTAATTCACCAAGATATTTCTACAGTTTCAATTCCTTAAACAAACAGA 1475
Db 4100 ACGATAATTTCCAAAGTTTAAACCAAGATATATTGCGAGTTTAAATTTCTTAAACCAACAT 4041
QY 1476 GGTATAAATTTGGGAGTATTCCTTACCAATTTAAGCAGACACAAATTTAAACAAAGTGG 1535
Db 4040 CCTATAAATATATGGTAATATACCTTATAACATAAGTACGGATATTAATACGCAAAATTG 3981
QY 1536 TTTTITGAAGCCATCGCTCTCACATCTATCTGATTGTTGAAGAGGATTTCTACAAGCGTA 1595
Db 3980 TTTTITGATAGTATAGCTAATCAGATTTATTTAATCGTGAATACGGGTTTTCGCTAAAGAT 3921
QY 1596 CTTTGGATATTCACGGAACACTAGGTTGCTCTTGACACTCAAGTCTCGATTCAGCAAT 1655
Db 3920 TATTAAATACAAAACGGCTCATTTGCTGATTTCTTAAATGGCAGAGTTGATTTCTTATAT 3861
QY 1656 TGCTTAAGCTCCCGCGGAATGCTTTCATCTTAAACCAAAAGTAAACAGAGTCTTAAATAA 1715
Db 3860 TAAGTATGGTCCAAAGAGATATTTTCTTAAACCTTAAAGTGAATAGCTCACTATCA 3801
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Db 3800 GATTAAAGTAGAAAAAATCAAGATATATCACAAAGATAAACAAAGTAAATATTTCG 3741
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QY 1836 CAATGAACACGCCAAAGTAAACAAATTTAAGTACCGTTTACTTATGCAAGATTTGCTTA 1895
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RESULT 15

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US-08-875-154-2/c
; Sequence 2, Application US/08875154
; Patent No. 5882888
; GENERAL INFORMATION:
; APPLICANT: Jorgensen, Streen Troels
; TITLE OF INVENTION: DNA Integration By Transporation
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5882888 No. 5882888disk of No. 5882888th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,154
; FILING DATE: 17-JUL-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4381.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-857-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6169 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "psj2739"
; ORIGINAL SOURCE:
; ORGANISM: psj2739
; US-08-875-154-2

Query Match
Best Local Similarity 58.0%; Pred. No. 4.2e-44;
Matches 432; Conservative 0; Mismatches 313; Indels 0; Gaps 0;

QY 1176 AATTAAAGAGGAGTCAATACATGAACAAAAATATAAAAAATTTCTCAAAACCTTTTAAACA 1235
Db 1539 AATTAAAGAGGTTATATATGACGAGAAAAATATAAAACACAGTCACAACTTTTACTT 1480
QY 1236 GTGAAAAAGTACTCAACCAATATAATAAACAATTTGAATTTAAAGAAACCGATACCGTTT 1295
Db 1479 CAAAACATAATATAGATAAAATATGACAAATATAAGATTAAGATGAACATGATATATCT 1420
QY 1296 ACGAATTTGGAACAGGTAAGGCAATTTAAACGACGAPACTGCTAAATAAAGTAAACAGG 1355
Db 1419 TTGAAATCGGCTCAGAAAGGCCAATTTTACCTTTGAATTTAGTAAAGAGGTGTTATTCG 1360
QY 1356 TTAACGTCTTATGAATTAGACAGTCTCATCTATTCAACTTATCTGTCAGAAAAATTTAAAC 1415
Db 1359 TTAACGTCCATTTGAATATAGACCAATAAATTTATGCAAACTTACAGAAAAATTAACCT 1300
QY 1416 ATACTCGTGTCACTTTAATTCACCAAGATATTTCTACAGTTTCAATTCCTTAAACAAACA 1475
Db 1299 ACGATAATTTTCAAGTTTAAACAAAGGATATTTGCGAGTTTAAATTTTCTTAAACCAAT 1240
QY 1476 GGTATAAATTTGTCGGAGTATTCCTTACCAATTTAAAGCAGACAAATTTATTTAAACAG 1535
Db 1239 CCTATAAATATATGTTAATATACCTTATAACAATAAGTACGGATATAATACGCAAAAT 1180
QY 1536 TTTTGAAGCCATCGCTCTGACATCTATCTGATTTGTTGAAGAGGATTTCTACAGCGTA 1595
Db 1179 TTTTGTAGTATAGCTAATGAGATTTTAAATCGTGAATACGGGTTTCTGCTTAAAGAT 1120
QY 1596 CCTGTGATATTCACCGAACACTTAGGTTTCTTCTGACACTCAAGTCTCGATTTCAGCAAT 1655
Db 1119 TATTAAATACAAACGCTCATTTGGCATTTCTTTAATGCGAGAGTTGATATTTCTATAT 1060
QY 1656 TCGTTAAGCTGCCAGCGGAATGCTTTTCACTTAAACCAAAAGTAAACAGTGTCTTAAATAA 1715
Db 1059 TAAATGTTGTTTCCAAAGAGATATTTTCTATCTTAAACCTTAAAGTGAATAGCTCACTT 1000
QY 1716 AACTTACCGCCATACACAGATGTTCCAGATAAATATTGGAAGCTATATACGTACTTTG 1775
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QY 1776 TTTCAAAATGGGTCAATCGAGAATATCGTCAACTGTTTCTTAAACCAAGTGTCTTCAAG 1835
Db 939 TTATGAATGGTTTAAACAAAGATTAACAGAAAAATTTTACAAAAATCAATTTAACCAAT 880
QY 1836 CAATGAACACGCCAAAGTAAACAAATTTAAGTACCGTTTACTTATGAGCAAGTATTGCTTA 1895
Db 879 CTTTAAACATGCAAGGATTTGACGATTTAAACATATTAGCTTTGAACAAATTTCTATCTC 820
QY 1896 TTTTAAATAGTATCTATTATTAA 1920
Db 819 TTTTCAATAGCTATAAATTTTAA 795

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Search completed: September 2, 2004, 00:17:01
Job time : 342 secs